GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

December 19, 2002, 16:41:38 ; Search time 33 Seconds (without alignments) 26.218 Million cell updates/sec

US-09-692-401-4 46 Title: Perfect score:

1 VRIGHLYIL 9

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

789 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 9

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database:

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	COI intron 16 prot		litorin I - Austra	D-amino-acid oxida	carbon-monoxide de	phosphonoacetaldeh	Iq heavy chain CRD	growth-modulating	sarcosine dehydrod	collagen alpha 1(ī	hypothalamic hepta	gramicidin S synth	1	litorin - Rohde's	T-cell receptor be	fatty-acid synthas		sex pheromone cAM3	hypothetical L2 pr	ribosomal protein	gamma subunit of P	N-formyl oliqopept	microcin C7 - Esch	serum albumin - do	telomeric and tetr	coat protein beta	sperm-activating p	kidney and bladder	dextransucrase (EC
										•																					
		Ω	138888	S07205	S07204	S39437	PL0140	A28709	PT0238	GKHU	A61419	B56979	NYPG7	S42407	A61467	S07241	PT0721	A60139	PQ0663	A25269	I56695	S78420	A48360	A60986	S45311	B45800	PC4373	S13636	JN0026	G58502	B39841
		DB	7	~	~	~	~	~	N	c	7	7		7	7	7	7	~	7	7	4	~	7	~	7	~	~	~	7	~	7
		Length	4	σ	6	σ	4	7	6	e	9	9	7	7	80	6	4	7	7	7	7	6	4	φ	7	8	80	6	6	6	6
ф	Query	Match	37.0	7	7	7	ď.	ď.	32.6	30.4	30.4	30.4	30.4	30.4	30.4	30.4	28.3	28.3	28.3	28.3	28.3	28.3	26.1	26.1	26.1	26.1	26.1	26.1	26.1	26.1	26.1
		Score	17	17	17	17	15	15	15	14	14	14	14	14	14	14	13	13	13	13	13	13	12	12	12	12	12	12	12	12	12
	Result	No.	-	2	m	4	S	φ	7	ω.	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

RESULT 2 S07205

SU/ZOL Litorin 2-Glu - Australian tree frog (Litoria aurea)
C; Species: Litoria aurea
C; Deteies: Litoria aurea
C; Deteies: Litoria aurea
C; Deteies: 12-Feb-1993 #sequence\_revision 12-Mar-1993 #text\_change 18-Aug-2000
C; Accession: S07205
R; Anastasi, A.; Montecucchi, P.; Angelucci, F.; Erspamer, V.; Endean, R.
Experientia 33, 1288, 1977
A; Title: Glu(OMe) (2)-litorin, the second bombesin-like peptide occurring in methanol
A; Reference number: S07205; MUID:78003546; PMID:908397
A; Accession: S07205
A; Molecule type: protein
A; Residues: 1-9 <ANA>
C; Superfamily: gastrin-releasing peptide
C; Sepwords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F; 1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F; 9/Modified site: amidated carboxyl end (Met) #status experimental

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Gaps ; 0

Ouery Match 37.0%; Score 17; DB 2; Length 9; Best Local Similarity 66.7%; Pred. No. 2.8e+05; Matches 2; Conservative 1; Mismatches 0; Indels

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30 11 23.9 5 2 PO0009 31 11 23.9 5 3 JT0870 32 11 23.9 7 2 S71867 33 11 23.9 7 2 S08606 34 11 23.9 7 2 S08606 35 11 23.9 7 2 S18797 36 11 23.9 7 2 S18797 37 11 23.9 7 2 S18797 38 11 23.9 8 2 PH0618 39 11 23.9 8 2 PH0618 41 12 23.9 8 2 PH0618 42 11 23.9 8 2 PH1618 43 11 23.9 8 2 PH1618 44 11 23.9 9 2 A91476 44 11 23.9 9 2 A93147 45 11 23.9 9 2 A93148 ALIGNMA C.Coccession: 13888 4.Accession:
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C;Species: Bacillus cereus
C;Species: 22-Aug-1988 #sequence_revision 22-Aug-1988 #text_change 30-Sep-1993
C;Accession: A28709
R;Olsen, D.B.; Hepburn, T.W.; Moos, M.; Mariano, P.S.; Dunaway-Mariano, D.
Biochemistry 27, 2229-2234, 1988
A;Title: Investigation of the Bacillus cereus phosphonoacetaldehyde hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           growth-modulating peptide - human
Cippecies: Homo sapiens (man)
Cipacies: Homo sapiens (man)
Cipacie: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
Cipaciesine: A01421
Rischlesinger, D.H.; Pickatt, L.; Thaler, M.M.
Rischlesinger, D.H.; Pickatt, L.; Thaler, M.M.
A;Title: Growth-modulating serum tripeptide is glycyl-histidyl-lysine.
A;Reference number: A01421; MUID:77162369; PMID:858356
A;Accession: A01421
A;Nolecule type: protein
                                                                                               Score 15; DB 2; Length 4;
Pred. No. 2.8e+05;
1; Mismatches 0; Indels
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Pred. No. 2.8e+05;
3; Mismatches 1; Indels
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A;Accession: A28709
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40.0%; Pred. No. 2.8e+05;
live 1; Mismatches 2;
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                                                                                          Query Match 32.6%;
Best Local Similarity 66.7%;
Matches 2; Conservative
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Best Local Similarity 33.2
Est Local 2; Conservative
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C; Keywords: oxidoreductase
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A;Molecule type: protein
A;Residues: 1-7 <OLS>
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Matches 2; Conserv
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4 VDHSY 8
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1 LKIDHV (
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1 MGH 3
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D-3443/

C;Species: Trigonopsis variabilis

C;Species: Trigonopsis variabilis

C;Species: Trigonopsis variabilis

C;Species: Trigonopsis variabilis

C;Species: 19-Mar-1997 #sequence_revision 05-Dec-1997 #text_change 07-May-1999

C;Accession: 839437

R;Schraeder, T; Andreesen, JR.

R;Schraeder, JR.

R;Schraeder
                                                                                                                                                                                                                                                                                                                         C:Species: Litoria aurea aurea control variable aurea control in the control aurea composition and sequence of litorin, a bombesin-like nonapeptide from A: Respecientia 31, 510-511, 1975

A:Ancession: S07204

A:Ancession: S07204

A:Ancession: S07204

A:Ancession: S07204

A:Ancession: S07204

A:Ancession: S07204

C:Superfamily: gastrin-releasing peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      carbon-monoxide dehydrogenase (EC 1.2.99.2) large chain - Pseudomonas carboxydohydrogen
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                                                                                                                                                                                                                                                                                                   litorin I - Australian tree frog (Litoria aurea)
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A; Molecule type: protein
A; Residues: 1-4 <KRA>
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2 VGH 4
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5 VGH 7
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VGH
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Gaps

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gramicidin S synthetase component II - Bacillus brevis (fragment)
C;Species: Bacillus brevis
C;Species: Bacillus brevis
C;Species: 20-oct-1994 #sequence_revision 12-Apr-1996 #text_change 12-Apr-1996
C;Accession: $43407
R;Stein, T.; Vater, J.; Kruft, V.; Wittmann-Liebold, B.; Franke, P.; Panico, M.; Mc D FRBS Lett. 340, 39-44, 1994
A;Title: Detection of 4'-phosphopantetheine at the thioester binding site for L-valin A;Reference number: $42407; MUID:94164305; PMID:8119405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 penalbumin - Adelie penguin (fragment)
C;Species: Pygoscelis adelie (Adelie penguin)
C;Species: Pygoscelis adelie (Adelie penguin)
C;Date: 07-06r-1994 #sequence_revision 04-Nov-1994 #text_change 04-Nov-1994
C;Accession: A61467
R;Osuga, D.T.; Aminlari, M.; Ho, C.Y.K.; Allison, R.G.; Feeney, R.E.
J. Protein Chem. 2, 43-62, 1983
A;Title: Sulfhydryl proteins of penguin egg white: ovalbumin and penalbumin. Comparis A;Accession: A61467
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litorin - Rohde's leaf frog

litorin - Rohde's leaf frog

C;Specias: Pyllomedusa rohdei (Rohde's leaf frog)

C;Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 18-Aug-2000

C;Accession: S07241

R;Barra, D.; Falconieri Erspamer, G.; Simmaco, M.; Bossa, F.; Melchiorri, P.; Erspame
FEBS Lett. 182, 53-56, 1985

A;Title: Rohdei-litorin: a new peptide from the skin of Phyllomedusa rohdei.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 1-8 <OSU>
C;Comment: Penalbumin is a major protein component of egg whites from penguins but
C;Keywords: egg white; glycoprotein
                                                                                                                                                                                                                  Score 14; DB 1; Length 7;
Pred. No. 2.8e+05;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.4%; Score 14; DB 2; Length 7; 100.0%; Pred. No. 2.8e+05; Live 0; Mismatches 0; Indels
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      A;Reference number: A01417; MUID:81213980; PMID:6263778
A;Accession: A01417
A;Molecule type: protein
A;Residues: 1-7 < CHA>
C;Superfamily: hypothalamic heptapeptide
C;Keywords: hypothalamus
                                                                                                                                                                                                            Query Match 30.4%;
Best Local Similarity 60.0%;
Matches 3; Conservative
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Best Local Similarity 50.09
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Conservative
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Matches 2; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothalamic heptapeptide - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Ol.Sep-1981 #sequence_revision 01-Sep-1981 #text_change 23-Aug-1996
C;Accession: A01417
R;Chang, R.C.C.; Huang, W.Y.; Arimura, A.; Redding, T.W.; Coy, D.H.; Saffran, M.; Kong,
Horm. Metab. Res. 13, 228-232, 1981
A;Title: Isolation, structure and synthesis of a heptapeptide with in vitro ACTH-releasi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-6 <WUA>
A;Note: the residue designated "X" is modified Lysine in collagen 1(II) some cross-linke
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Nylternate names: collagen alpha 3(XI) chain
Cispecies: Bos primigenius taurus (cattle)
Cibate: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 03-Oct-1995
CiAccession: B56979
Riwu, 7.J.: Eyre, DR.
Dialol. Chem. 270, 18865-18870, 1995
A; Title: Structural analysis of cross-linking domains in cartilage type XI collagen.
                           A;Note: this serum tripeptide is found to stimulate growth of some cell types and C;Superfamily: unassigned animal peptides
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A,Residues: 1-6 <PIN>
C;Keywords: FAD: flavoprotein; oxidoreductase; phosphoprotein
F;6/Modified site: 3'-FAD-histidine (His) #status experimental
                                                                                                         Query Match 30.4%; Score 14; DB 3; Length 3; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 2; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
30.4%; Score 14; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels
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30.4%; Score 14; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels
A; Residues: 1-3 <SCH>
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Total receptor beta chain V-D-J region (140-2K) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0721
S;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0721
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28.3%; Score 13; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels
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Search completed: December 19, 2002, 16:45:39 Job time : 34 secs

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2 RIG 4

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ALIGNMENTS

P38644 m P81337 c P81337 c P82992 p P19823 c P80027 p P31929 p P19149 s P42562 p P52997 c P52997 c P01373 p P01373 p

UF06\_MOUSE BUK\_CLOPA IPYR\_RHOVI MOSF\_CIT/JA OXYT\_OCTVU ULAD\_HUWAN XYLA\_STRSO EOSI\_HUWAN FYRI\_ANTEL FYRI\_ANTEL BIOB\_CITFR PRCT\_PERAM

8000000044400 1111111111111

221.7 221.7 221.7 221.7 221.7 19.6 19.6 19.6

clostridium rhodopseudo

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December 19, 2002, 16:40:38; Search time 10 Seconds (without alignments) 37.329 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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46
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Perfect score:
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	Description	1 -			P41492 sarcophaga	pseno	P01157 homo sapien	ascar	P01153 sus scrofa	P08946 phyllomedus	_		P81179 diaprepes a		P19852 clypeaster		O68936 serratia ma	P41853 artioposthi	daucus	P81675 pinus pinas	cydia	_		scylio	P42999 squalus aca		-	_		0	P54714 canis famil	P38639 mus musculu	P41966 moniezia ex	564 hirudo m	P18691 thunnus alb
SUMMARIES	ID	THE TOTAL	LITO_LITAU	NEUX_HUMAN	NSKI_SAKBU	DCML_PSECH	GRWM_HUMAN	FAR2_ASCSU	HY7_PIG	LITR_PHYRO	CIA_ENTFA	GFRP_MOUSE	PGLR_DIAAB	ANG2_BOTJA	MOSH_CLYJA	RE42_LITRU	RS10_SERMA	FARP_ARTTR	PSK_DAUCA	UNO6_PINPS	ALL6_CYDPO	ISOT_CYPCA	NEUU_CAVPO	OXYA_SCYCA	OXYA_SQUAC	OXYT_BUFRE	OXYT_CYPCA	OXYT_RABIT	OXYT_RAJCL	OXYV_SQUAC	TPIS_CANFA	UF01_MOUSE	FARP_MONEX	FAR5_HIRME	ACI_THUAL
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01-FBS-1994 (Rel. 28), Least sequence update) 10.7-RD-1994 (Rel. 28), Least sequence update) 11.0-JUN-2002 (Rel. 41, Last annotation update) 12.0-JUN-2002 (REPHYLATE) 13.150-511(1975). 12.0-JUN-2002 (RETHYLATE) 13.150-511(1975). 13.150-151(1975). 14.0-JUN-2002 (RETHYLATE) 14.0-JUN-2002 (RETHYLATE) 15.0-JUN-2002 (RETHYLATE) 16.0-JUN-2002 (RETHYLATE) 17.0-JUN-2002 (RETHYLATE) 18.0-JUN-2002 (RETHYLATE) 19.0-JUN-2002 (REL. 41, MANOTACHIOR) 19.0-JUN-2002 (REL. 41, MAN	<u>م</u> ح	P08945;			- TO				
15-JUN-2002 (Rel. 41, Last annotation update) Litoria aurea (Green and golden bell frog). Enkaryota: Metacada: Choddata: Craniata: Vertebrata: Eutoleostomi; Puldoria aurea (Green and golden bell frog). Enkaryota: Metacada: Choddata: Craniata: Vertebrata: Eutoleostomi; Puldoria aurea (Incorda: Neobatrachia: Bufonoidea: Hylidae; NCBI_TAXID=871; SEQUENCE: Anastasia A. Erspamer V. Endean R.; Anastasia A. Erspamer V. Endean R.; Litoria aurea (Incorda: Composition and sequence of litorin, a bombesin-like promappelitide from the skin of the Australian leptodactylid frog Litoria aurea.) Experientia 31:510-511(1975). Experientia 31:120-1219(1977). Experientia 31:120-1289(1977). Experientia 33:120-1289(1977). Experienti		1-FEB-1994				update)			
Litoria aurea (Green and golden bell frog).  Eukaryota whetazoa; Chordata; Vertebrata; Euteleostomi;  Pelofityaniae; Intoria.  NCBL TaxID-8371;  MEDLINE-75187011; PubMed-1140241;  Anatata; A. Erspamer V., Endean R.;  Anatata; A., Erspamer V., Endean R.;  Anatata; A., Montecucchi P.C., Anatalian leptodactylid frog Experientia 31:510-511(1975).  Experientia 31:510-511(1975).  SEQUENCE (METHYLATED VARIANT).  MEDLINE-78003546; PubMed-908337;  Anatata; A., Montecucchi P.C., Anatalian leptodactylid frog Experientia 31:510-511(1975).  Experientia 31:510-511(1975).  SEQUENCE (METHYLATED VARIANT).  MEDLINE-78003546; PubMed-908337;  Anatatasi A., Montecucchi P.C., Anatataian frog Litoria aurea.  "Glu(OMe) 3-11torin, the second bombesin-11ke peptide occurring in  Experientia 33:1289-1289(1977).  "Glu(OMe) 3-11torin, the second bombesin-11ke peptide occurring in  Experientia 33:1289-1289(1977).  "T. SUBCELLUAR LOCATION: Secreted.  "T. SUBCELLUAR LOCATION: Secreted.  "T. SUBCELLUAR LOCATION: Secreted.  "T. SOTO25; SOTO36.  InterPro: IPRO00874; Bombesin.  PERMITY.  PREMITY TY: BELONGS TO THE BOMBESIN/NEUNEUMEDIN B/RANATENSIN  PIR: SOTO25; SOTO36.  InterPro: IPRO00874; Bombesin.  PERMITY IN BELONGS TO THE BOMBESIN/NEUNEUMEDIN B/RANATENSIN  PRAMITY IN BELONGS TO THE BOMBESIN/NEUNEUMEDIN B/RANATENSIN  PROJEES 2 2 METHYLATION.  MOD_RES 2 2 METHYLATION  SEQUENCE 9 AA; 1103 MW; DTCCLEB62CDC366 CRC64;  DUELY MACCh  SEQUENCE 9 AA; 1103 MW; DTCCLEB62CDC366 CRC64;  SUBCITE 2  SUBCELLUAR LOCAL Similarity 66.7%; Pred. No. 1.1a+05;  MULL 2  MEULT 3  ME	DE L	5-JUN-2002 itorin				n update		•	
Eukaryota; Wetazoa; Chordata; Oranjata; Vertebrata; Euteleostomi; Pelodryadinae; Litoria.  NUBL_TaxID-837;  (NIBL_TaxID-837);  (NIBL_TaxID-837);  (NIBL_TaxID-837);  (NIBL_TaxID-837);  (NIBLINE-758701]; PubMed=1140241;  Anastasi, A., Erspamer V., Endean R.;  Ananinoacid composition and sequence of litorin, a bombesin-like nonapeptide from the skin of the Australian leptodactylid frog Litoria aurea.";  Experientia 31:510-511(1975).  (2)  (2)  (2)  (3)  (4)  (5)  (5)  (5)  (6)  (7)  (7)  (8)  (8)  (9)  (9)  (9)  (1)  (1)  (1)  (1)  (2)  (2)  (3)  (4)  (4)  (5)  (5)  (6)  (7)  (6)  (7)  (7)  (8)  (8)  (8)  (9)  (9)  (9)  (9)  (9		itoria aure	a (Gree	n and g	olden bell	frog).			
Amphiblia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae; Pelodryadinae; Litoria.  NEBLTaxID-8371; [11] EBQUENCE.  MEDLINE-7587011; PubMed=1140241; Anastasi A., Erspamer V., Endean R.; "Aminoacid composition and sequence of litorin, a bombesin-like nonapeptide from the skin of the Australian leptodactylid frog Litoria aurea.";  Experientia 31:510-511(1975).  [2] Experientia 31:510-511(1975).  [2] Experientia 31:510-511(1975).  [3] Anastasi A., Montecucchi P.C., Angelucci F., Erspamer V., Endean R. MEDLINE-7603546; PubMed=90839;  Anastasi A., Montecucchi P.C., Angelucci F., Erspamer V., Endean R. (*Cliv)(Mey 3-11torin, the second bombesin-like peptide occurring in methanol extracts of the skin of the Australian frog Litoria aurea. *I. SUBCELLUIAR LOCATION: Secreted.  -1. SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN FAMILY.  FRAMILY.  FRAMILY.  FRAMILY.  MOD_RES.  2 AMIDATION.  MOD_RES.  2 AMIDATION.  SEQUENCE GARGOUSTINE SOUGH.  SEQUENCE 9 AA: 1103 MW; DOCCCIR862CDC366 CRC64;  DUETY MATCH  SEQUENCE 9 AA: 1103 MW; DOCCCIR862CDC366 CRC64;  SEQUENCE 9 AA: 1103 MW; DOCCCIR862CDC366 CRC64;  SEGUENCE 9 AA: 1103 MW; Pred: No. 11e+05;  MULT 2  XLHMAN  MULT 2  XLHMAN  MULT 2  XLHMAN  MULT 2  XLHMAN  MULT 14  PROTECTION PROTEC		ukaryota; M	etazoa;	Chorda	ta; Crania	ta; Vert	ebrata; Eutele	ostomi;	
NCBL_TaxID=8371; SEQUENCE. MEDLINE-75187011; PubMed=1140241; Anastasia A. Erspamer V., Endean R.; Anastasia A. Erspamer V., Endean R.; Anastasia A., Erspamer V., Endean R.; Anastasia A., Erspamer V., Endean R.; Aninoacid composition and sequence of litorin, a bombesin-like nonapeptide from the skin of the Australian leptodactylid frog Litoria aurea.  [2] SEQUENCE (METHYLATED VARIANT), MEDLINE-78003546; PubMed=908397; Anastasia A., Montecucchi P.C., Angelucci F., Erspamer V., Endean R.; Anastasia A., Montecucchi P.C., Angelucci F., Erspamer V., Endean R.; Glu(OMe)3-11torin, the second bombesin-like peptide occurring in methanol extracts of the skin of the Australian frog Litoria aurea.  [2] SEQUENCE (METHYLATE) P.C., Angelucci F., Erspamer V., Endean R.; Anastasia A., Montecucchi P.C., Angelucci F., Erspamer V., Endean R.; FINILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN FRAILY.  PRES SOTOOS; SOTOOS. InterPro; IPRO0084; Bombesin; I. PROXIDE, Bombesin family; Amidation; Methylation.  MOD_RES J. MONBESIN; I. Bendesin family; Amidation; Methylation.  MOD_RES J. AMIDATION (IN A VARIANT).  MOD_RES J. AMIDATION (IN A VARIANT).  MOD_RES J. AMIDATION (IN A VARIANT).  MACHES J. AMIDATION (IN A MAINATION).  AALDATION (IN A MAINATION).  MACHES J. AMIDATION (IN A MAINATION).  AALORA (G.7%; Pred. No. 1.1.e+05; AAL	Æ (	mphibia; Ba	trachia	i; Anura	; Neobatra		fonoidea; Hyli	.dae;	
(1)   SEQUENCE.		elodryadına	e; Litc	ria.					
EXEQUENCE.  Amastasi A., Erspamer V., Endean R.;  Annastasi A., Erspamer V., Endean R.;  "Anthoacid composition and sequence of litorin, a bombesin-like nonapeptide from the skin of the Australian leptodactylid frog Litoria aurea.":  Experientia 31:510-511(1975).  [2]  EXPURING (METHYLATED VARIANT).  MEDLING-780033746; PubMed-908337;  Annastasi A., Montecucchi P.C., Angelucci F., Erspamer V., Endean R.  "Glu(OME) 31:10201. the second bombesin-like peptide occurring in methanol extracts of the skin of the Australian frog Litoria aurea. Experientia 33:1280-1289(1977).  "SEMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN FRAMILY:  FRAMILY: S07205; S07204.  PRES: S07205; S07204.  PRES: S07205; S07204.  PRES: PRO2044; Bombesin.  PROSITE: PS00057; BOMBESIN.  MOD_RES  2		CBL_TaxID=8	371;						
Anstasi A., Erspamer V., Endean R.; Anastasi A., Erspamer V., Endean R.; Anastasi A., Erspamer V., Endean R.; Anastasi A., Erspamer V., Endean R.; Anionacid composition and sequence of litorin, a bombesin-like nonapeptide from the skin of the Australian leptodactylid frog Litoria aurea.";  [2] Experientia 31:10-511(1975). [2] Experientia 31:20-511(1975). [3] EQUINE-78003546; Pubmed-908397; Anastasi A., Montecucchi P.C., Angelucci F., Erspamer V., Endean R. Gil(OMB)3-litorin, the second bombesin-like peptide occurring in methanol extracts of the skin of the Australian frog Litoria aurea."; [3] EQUINE-78003546; Pubmes Sin of the Australian frog Litoria aurea. Experientia 33:1289-1289(1977). [4] ENGINE SOCOSTOSTOSTOSTOSTOSTOSTOSTOSTOSTOSTOSTOSTO		I.J.							
Anastasi A., Erspamer V., Endean R.; Anastasi A., Erspamer V., Endean R.; Anastasi A., Erspamer V., Endean R.; Anantasi A., Enspamer V., Endean R.; Aninoacid composition and sequence of litorin, a bombesin-like nonapeptide from the skin of the Australian leptodactylid frog Litoria aurea.  Experientia 31:510-511(1975).  [2] SEQUENCE (METHYLATED VARIANT). Anastasi A., Montecuchi P.C., Angelucci F., Erspamer V., Endean R. "Glu(OMe)3-litorin, the second bombesin-like peptide occurring in methanol extracts of the skin of the Australian frog Litoria aurea.  "Glu(OMe)3-litorin, the second bombesin-like peptide occurring in Experientia 33:1289-1297).		EQUENCE. FOLTNE-7518	7011.	LPMOdu	140041.				
Aminoacid composition and sequence () litorin, a bombesin-like nonapeptide from the skin of the Australian leptodactylid frog Litoria aurea."  Experientia 31:510-511(1975).  SEQUENCE (METHYLATED VARIANT).  MEDLINE-78003546; PubMed-908397;  In Experientia 33:1289-1189(1977).  SEQUENCE (METHYLATED VARIANT).  PIR: 307204.  PIR: 307204; S07204.  PIR: 307205; S07205.  InterPro; IPMO0874; Bombesin. 1.  PORSITE; PS00257; BOMBESIN; 1.  MOD_RES 2 2 METHYLATION (IN A VARIANT).  MOD_RES 2 2 METHYLATION (IN A VARIANT).  MOD_RES 3 2 METHYLATION (IN A VARIANT).  SEQUENCE 9 AA; 1103 MM; D7CCCIE862CDC366 CRC64;  SEQUENCE 9 AA; 1103 MM; D7CCCIE862CDC36 CRC64;  SUBMESIN MATCH 66.7%; Pred. No. 1.1e+05;  MAIDATOR 0; INMOMEN OF PRED. 1.1 Mismatches 0; Indels 0; Gap 3 IGH 5  SULT 2  NEAL HUMAN STANDARD; PRT; 9 AA.		DDLINE-/JLO	TTTO/	upmed-1	T40241;				
nonapeptide from the skin of the Australian leptodactylid frog Litoria aurea.":  Experientia 31:510-511(1975).  [2]  Experientia 31:510-511(1975).  [2]  SEQUENCE (METHYLATED VARIANT).  MEDLINE-78003546; PubMed-908397;  Ansatasi A., Montecucchi P.C., Angelucci F., Erspamer V., Endean R., Glu(OMe) 3-11forin, the second bombesin-like peptide occurring in methanol extracts of the skin of the Australian frog Litoria aurea. Superientia 33:1289-1289(1977).  -: SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN FRMILY.  PIR: S07204; S07204.  PIR: S07205; S07205.  InterPro; IPROBOR A. Bombesin, PRRNICLIDONE CARBOXYLIC ACID. PROSITE; PS00257; BOMBESIN; 1.  Bombesin family, Amidation; Methylation.  MOD_RES 1 10 1 10 1 1 1 1 1 1 1 1 1 1 1 1 1 1		Mascasi A.,	Erspan	er v.,	Endean K.;	7,12		1111	
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Experientia 31:510-511(1975).  [2] [2] [2] [2] MEDLINE=7800346; PubMed=908397; MEDLINE=7800346; PubMed=908397; MEDLINE=7800346; PubMed=908397; Mensatasi A., Montecucchi P.C., Angelucci F., Erspamer V., Endean R., Glu(OMe)3-litorin, the second bombesin-like peptide occurring in methanol extracts of the skin of the Australian frog Litoria aurea.  [3] [2] [3] [4] [5] [5] [6] [6] [7] [7] [7] [8] [8] [8] [8] [8] [8] [8] [8] [8] [8		itoria aure		11140		רדמדדמוו	reproducty and	1109	
SEQUENCE (METHYLATED VARIANT).  SEQUENCE (METHYLATED VARIANT).  MEDLINE-7800346; Pubmed-90839;  Anastasi A., Montecucchi P.C., Angelucci F., Erspamer V., Endean R.  "Glu(OMe)3-11corin, the second bombesin-11ke peptide occurring in methanol extracts of the skin of the Australian frog Litoria aurea.  Experientia 33:1289-1289(1977).  -: SUBCLIULAR LOCATION: Secreted.  -: SINILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN PIR: S07205; S07205.  InterPro; IPRO00874; Bombesin. PRAMILY.  Bombesin.  PRAMILY.  AMIDATION.		xperientia	31:510-	511(197	5).				
SEQUENCE (METHYLATED VARIANT), MEDLINE=78003346; Pubmed=908397; Anastasi A., Montecucchi P.C., Angelucci F., Erspamer V., Endean R., Montecucchi P.C., Angelucci F., Erspamer V., Endean R., Glu(OMe)3-litorin, the second bombesin-like peptide occurring in methanol extracts of the skin of the Australian frog Litoria aurea.  "Glu(OMe)3-litorin, the second bombesin-like peptide occurring in methanol extracts of the skin of the Australian frog Litoria aurea.  Experientia 3:1289-1289(1977).	RN	2]		•					
MEDLINE-78003546; PubMed-908397; Anastasi A., Montecucchi P.C., Angelucci F., Erspamer V., Endean R. "Glu(OMe)3-11corin, the second bombesin-11ke peptide occurring in methanol extracts of the skin of the Australian frog Litoria aurea. Experientla 33:1289-1289(1977). Experientla 33:1289-1289(1977). EXPECTION SECONDER LOCATION: Secreted!- SUMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN PIR: S07204; S07204. PIR: S07204: S07204. PIR: S07205; S07205. InterPro: JPROUGNST4; Bombesin, 1. PROSITE; PS00257; BOMBESIN; 1. PROSITE; PS00257; BOMBESIN; 1. MOD_RES 1 METHYLATION (IN A VARIANT). MOD_RES 2 AMIDATION. MOD_RES 3 AMIDATION. MOD_RES 3 AMIDATION. MOD_RES 4 AMIDATION. MOD_RES 5 AMIDATION (IN A VARIANT). MOD_RES 6 AMIDATION. MOD_RES 7 AMIDATION. MOD_RES 7 AMIDATION. MOD_RES 9 AMIDATION. MOD		EQUENCE (ME	THYLATE	D VARIA	.VT).				
Anstasi A., Montecucchi P.C., Angelucci F., Erspamer V., Endean R. "Glu(Owe)3-litorin, the second bombesin-like peptide occurring in methanol extracts of the skin of the Australian frog Litoria aurea. Experientia 3:1289-128(1977).  - : SUBCELLULAR LOCATION: Secreted : SUMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN PIR; S07205; S07204. PIR; S07205; S07205. InterPro; IPRO00874; Bombesin. PRAMILY: PRO00874; Bombesin. PROSITE: PS00357; Bombesin. PROSITE: PS00357; Bombesin. PROSITE: PS00357; Bombesin. MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID. MOD_RES 2 AMIDATION. SEQUENCE 9 AA: 1103 MW; D7CCC1E862CDC366 CRC64; SEQUENCE 9 AA: 1103 MW; D7CCC1E862CDC366 CRC64; Best Local Similarity 66.7%; Pred. No. 1.1e+05; MALCHES 2; Conservative 1: Mismatches 0; Indels 0; Gap 3 IGH 5 3 IGH 7  SULT 2 3 MENANA STANDARD; PRT; 9 AA.		EDLINE=7800	3546; F	ubMed=9	08397;				
"Glu(OMe)3-liforin, the second bombesin-like peptide occurring in methanol extracts of the skin of the Australian frog Liforia aurea. Experientia 33:1289-1289(1977).  -!- SUBCELLULAR LOCATION: Secreted!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN PIR; S07204; S07204.  PIR; S07204; S07204.  PIR; S07204; Bombesin. 1.  PROSITE: PS0025; Bombesin. 1.  PROSITE: PS00257; Bombesin. 1.  PROSITE: PS00257; Bombesin. 1.  PROSITE: PS00257; Bombesin. 1.  PROSITE: PS00257; Bombesin. 1.  PS00257; Bom		nastasi A.,	Montec	ucchi F	.C., Angel	acci F.,	^	Endean R	٠.
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Experientia 33.1289-1289(1977).  -: SUBCELLULAR LOCATION: Secreted: SUMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN PIR; S07204; S07204.  PIR; S07205; S07204.  PIR; S07205; S07204.  PIR; S07205; S07205.  InterPro; IPR000874; Bombesin. PROSITE; PS00027; Bombesin. PROSITE; PS00027; Bombesin.  MOD_RES 1 NETHYLATION. MOD_RES 2 AMIDATION.  MOD_RES 9 9 AMIDATION.  SEQUENCE 9 AA; 1103 MW; D7CCIE862CDC366 CRC64;  SEQUENCE 9 AA; 1103 MW; D7CCIE862CDC366 CRC64;  MAIDATION.  SEQUENCE 9 AA; 1103 MW; D7CCIE862CDC366 CRC64;  SEQUENCE 9 AA; 1103 WW; D7CCIE862CDC366 CRC64;  SEQUENCE 9 AA; D7CCIE862CD		ethanol ext	racts c	f the s	kin of the	Austral	ian frog Litor	ia aurea	
-1- SUMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN PIR; SO7204; SO7204; SO7204. PIR; SO7204; SO7204. PIR; SO7204; SO7204. PIR; SO7205; SO7205. InterPro; IPRO00874; Bombesin. PROSITE; BF02044; Bombesin, 1. PROSITE; PS00057; Bombesin, 1. PROSITE; PS00067; Bombesin, 1. PROSITE; PS00057; Bombesin, 1. PROSITE SOTO Bombes		xperientia	33:1289	-1289(1	977).				
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Program; PF02044; Bombosin. Program; PF02044; Bombosin. Bombosin family; Amidation; Methylation. MOD_RES 2 2 AMIDATION. MOD_RES 3 9 AMIDATION. SEQUENCE 9 AA; 1103 MW; D7CCIE662CDC366 CRC64; Diest Matches 2; Conservative 1; Mismatches 0; Indels 0; 3 IGH 5 3 IGH 5 5 VGH 7  METHYLATION (IN A VARIANT). METHYLATIO		1K; 50/205;	207/08		1				
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PROBLIE; PSU025); BOMBESIN; 1.  BOMDESIN family; Amidation; Methylation.  MOD_RES 2 NETHYLATION (IN A VARIANT).  MOD_RES 9 9 AMIDATION.  SEQUENCE 9 AA: 1103 MW; DACCIEGGSCOC366 CRC64;  Query Match 37.0%; Score 17; DB 1; Length 9; Best Local Similarity 66.7%; Pred. No. 1.1e+05;  Matches 2; Conservative 1; Mismatches 0; Indels 0; 11 S VGH 7  SULT 2  UX_HUMAN STANDARD; PRT; 9 AA.		ram; PF0204	4; Bomb	esin; l					
### Bonnesin family; Amidation; Methylation of PyrroLidone Carboxylic ACID.  ###################################			0257; B	OMBESIN					
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MOD_RES 9 AND ANIDATION.  SEQUENCE 9 AA; 1103 MW; D7CCIE862CDC366 CRC64;  Query Match 37.0%; Score 17; DB 1; Length 9;  Best Local Similarity 66.7%; Pred. No. 1.1e+05;  Matches 2; Conservative 1; Mismatches 0; Indels 0;  3 1GH 5 3 1GH 5 5 VGH 7  SULT 2  3X_HUMAN STANDARD; PRT; 9 AA.		OD_RES	7	7	METHYLA		A VARIANT).		
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Duery Match 37.0%; Score 17; DB 1; Length 9; Best Local Similarity 66.7%; Pred. No. 1.1e+05; Matches 2; Conservative 1; Mismatches 0; Indels 0; 3 IGH 5 :			AA;	103 MW;		52CDC366	CRC64;		
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5 VGH 7 SULT 2 UX_HUMAN NEUX_HUMAN STANDARD; PRT; 9		-							
SULT 2 JX_HUMAN NEUX_HUMAN STANDARD; PRT; 9		VGH							
PO4277;	SULT	22							
P042//;	{	EUX_HUMAN	STAN	DARD;	PRT;				

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Score 16; DB 1; Length 9; Pred. No. 1.1e+05;
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-!- FUNCTION: MYOTROPIC PEPTIDE.
-!- SINLARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY. INCAPLO: IPR001651; Gastrin.
PROSITE; PS00259; GASTRIN; I.
                                                                                                                                                                                              "The amino acid sequence of kinetensin, a novel peptide isolated from
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01-NOV-1995 (Rel. 32, Last sequence update)
01-RDS-1996 (Rel. 33, Last annotation update)
01-FEB-1996 (Rel. 33, Last annotation update)
Neosulfakinin-I (NEB-SK-I).
Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Oestroidea; Sarcophagidae; Sarcophaga.
                                                           Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606, 9913, 9986;
                                                                                                                                                                                                                                                                        SPECIES-Human, Bovine, and Rabbit;
MEDINE-87194805; PubMed-243111;
Carraway R.E., Mitra S.P., Cohrane D.E.;
Structure of a biologically active neurotensin-related peptide obtained from pepsin-treated albumin(s).";
J. Biol. Chem. 263:5968-5973(1987).
-I-FUNCTION: REGULATION OF FAT DIGESTION, LIPID ABSORPTION, AND PIR, A03239; ABHUSR.
PIR, A26693; A26693.
                                                                                                                                                        MEDLINE-86242180; PubMed=3087352;
Mogard M.H., Kobayashi R., Chen C.F., Lee T.D., Reeve J.R. Jr.,
Shively J.E., Walsh J.H.;
                                                                                                                                                                                                       pepsin-freated human plasma: homology with human serum albumin, neurotensin and angiotensin."; Biochem. Biophys. Res. Commun. 136:983-988(1986),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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4 SULFATION (POTENTIAL).

MOD RES 9 AMIDATION (POTENTIAL).

SEQUENCE 9 AA; 1187 MW; 8B0A0691E86B5AAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     9 AA; 1172 MW; C804DB4761F4140D CRC64;
20-MAR-1987 (Rel. 04, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Neurotensin-related peptide (NRP) (Kinetensin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              34.8%;
60.0%;
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                                                   Bos taurus (Bovine), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                        Homo sapiens (Human),
                                                                                                                                             SPECIES-Human;
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NSK1_SARBU
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--- COFACTOR: Molybdenum (molybdopterin).
--- SUBDNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schlesinger D.H., Pickart L., Thaler M.M.;
Schlesinger D.H., Pickart L., Thaler M.M.;
"Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";
"Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";
-1- MISCELLANEOUS: THIS SERUM TRIPEPTIDE HAS BEEN FOUND TO STIMULATE
GROWTH OF SOME CELL TYPES AND TO INHIBIT OTHER TYPES IN VITRO.
SEQUENCE 3 AA; 340 MW; 6331E81000000000 CRC64;
Gaps
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Bradyrhizobium group.
NCBI_TaxID=290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kraut M., Hugendieck I., Herwig S., Meyer O.;
"Homology and distribution of CO dehydrogenase structural genes
carboxydotrophic bacteria."
Arch. Microbiol. 152:335-341(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
0;
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                                                                                                                                                                                                                                                                                                                                         01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO dehydrogenase subunit L) (CO-DH L) (Fragment).
0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 4;
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21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last sequence update)
Growth-modulating peptide.
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   1; Mismatches
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Phyllomedusa rohdei (Rohde's leaf frog).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000874; Bombesin.
Pfam; PF02044; Bombesin; 1.
PROSITE; PS00257; BOMBESIN; 1.
                                                                                                    30.4%;
60.0%;
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les 2; Conservative
                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                         STANDARD;
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Best Local Similarity
"-hes 3; Conserve
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MOD_RES
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present in the Rhabditida).";
                                                 Gaps
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NCBL_TaxID=6253, 6233;
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
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MEDLINE-81213980; PubMed-6263778;
Chang R.C.C., Huang W.-Y., Arimura A., Redding T.W., Coy D.H.,
Saffran M., Kong A., Hamilton J.W., Cohn D.V., Schally A.V.;
                                                                                                                                                                                                                                                                                  FMRFamide-like neuropeptide AF2.
Ascaris suum (Pig roundworm) (Ascaris lumbricoides), and
                                             Indels
               Length 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 14; DB 1; Length 7; Pred. No. 1.1e+05; 1; Mismatches 1; Indels
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            Score 14; DB 1; Le
Pred. No. 1.1e+05;
0; Mismatches 0;
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(Rel. 26, Last sequence update)
(Rel. 33, Last annotation update)
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30.4%; Scor
100.0%; Pre
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21-JUL-1986 (Rel. 01, Last seqt
21-JUL-1986 (Rel. 01, Last anno
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                                               Conservative
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                                                                                                                                                                                                   STANDARD;
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                            Best_Local Similarity
Matches 2; Conserv
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01-FEB-1996
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GH 2
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P01153;
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peptide from the skin of Phyllomedusa rohdei.";
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MEDLINE-87005252; PubMed-3093276;
MOTI M., Tanaka H., Sakagami Y., Isogai A., Fujino M., Kitada C.,
Moti B.A., An F.Y., Clewell D.B., Suzuki A.;
"Isolation and structure of the Streptococcus faecalis sex pheromone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           p11932;
01-0071-1989 (Rel. 12, Created)
01-077-1989 (Rel. 12, Last sequence update)
01-FBB-1991 (Rel. 17, Last annotation update)
Sex pheromone CAM373 (Clumping-inducing agent) (CIA).
Enterooccus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCBI_TaxID=1351;
                                                                                                                                                                                                                                                                        Gaps
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"Isolation, structure and synthesis of a heptapeptide with in vitro ACTH-releasing activity from porcine hypothalamus.";
Horm. Metab. Res. 13:228-232(1981).
PIR; A01417; NY607.
SEQUENCE 7 AA; 957 MW; 632845B1FB5059A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
Phyllomedusinae; Phyllomedusa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barra D., Erspamer G.F., Simmaco M., Bossa F., Melchiorri P., Erspamer V.; "Rohdei-litorin: a new peptide from the skin of Phyllomedusa rol FEBS Lett. 182:53-56(1985).
-! - SUBCELLULAR LOCATION: Secreted.
-! - SUBCELLULAR LOCATION: TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
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0
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Pred. No. 1.1e+05;
0; Mismatches 2; Indels
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9 AA; 1090 MW; 4ECCC1E861ADC377 CRC64;
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100.0%; Pred. No. 1.1e+05;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1988 (Rel. 09, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
hodel-litorin.
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TISSUE=Plasma;
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2 YTYVI 6
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3 VYI 5
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Q10582;
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ID MOSH_CLYJA
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      SEOUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P19852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANG2_BOTJA
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      δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                             QQ
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                                                                                                                                                                                                                                                             Gaps
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-!- FUNCTION: MEDIATES TETRAHYDROBIOPTERIN INHIBITION OF GTP
CYCLOHYDROLASE I. THIS INHIBITION IS REVERSED BY L-PHENYLALANINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 47, Last annotation update)
15-JUN-2094 (Rel. 47, Last annotation update)
15-JUN-2094 (Rel. 47, Last annotation update)
15-JUN-2094 (Rel. 47, Legendary (Rel. 47, Rel. 47
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15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
GTP cyclohydrolase I feedback regulatory protein (P35) (Fragment).
GCHFR OR GFRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                          -!- MISCELLANEOUS: THE N-TERMINUS IS POSSIBLY RESPONSIBLE FOR SPECIFICITY OF PHEROMONES TO PLASMIDS.
-!- SIMILARITY: C-FERMINAL TO THE PHEROMONES CPD1 AND CAD1.
PIR; A25269; A25269.
CAM373.";
FEBS Lett. 206:69-72(1986).
-!- FUNCTION: CAM373 INDUCES MATING RESPONSE OF DONOR CELLS
HARBORING PAM373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Liver;
Sanchez J.-C., Rouge V., Frutiger S., Hughes G., Yan J.X.,
Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,
                                                                                                                                                                                                                  Score 13; DB 1; Length 7; Pred. No. 1.1e+05; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.3%; Score 13; DB 1; Length 7; 66.7%; Pred. No. 1.1e+05; tive 1; Mismatches 0; Indels
                                                                                                                                                                             75BDD72059C05DB0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         7 AA.
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-!- SUBUNIT: HOMODINER (BY SIMILARITY).
SWISS-2DPAGE: P99025; MOUSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                      28.3%;
50.0%;
                                                                                                                                                                             7 AA; 734 MW;
                                                                                                                                                                                                                    Query Match 28.3 Best Local Similarity 50.0 Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Matches 2; Conserv
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NCBI_TaxID=13040;
[1]
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IFIL 5
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P99025;
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P81179;
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                                                                                                                                                          Pheromone.
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SEQUENCE
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1D PGLR_D
AC P81179
DT 15-JUL
DT 15-JUL
DT 15-JUL
DT 15-JUL
OC BURSTY
OC BURSTY
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CO DIABRE
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TISSUE-Larval gut;

Doostdar H., McCollum T.G., Mayer R.T.;

"Purification and characterization of an endo-polygalacturonase from "Purification and characterization of an endo-polygalacturonase from bure gut of West Indies sugarcane rootstalk borer weevil (Diaprepes abbreviatus L.) larvae.",

Comp. Biochem. Physiol. 118B:861-867(1997).

-!-CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-galactosiduronic linkages in pectate and other galacturonans.
-!-INDUCTION: INHIBITED BY CITRUS PGIP.
-!-MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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"Isolation and identification of angiotensin-like peptides from the
plasma of the snake Bothrops jararaea.";
Comp. Biochem. Physiol. 1138:467-473(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordatá; Craniata; Vertebrata; Euteleostomi;
Epidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.
NCBL_TaxID=8724;
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 13; DB 1; Length 9; Pred. No. 1.1e+05; 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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                                                                                                                                                                                                                                                                                                                                                                   9 AA; 1041 MW; 1F49087042DB41BB CRC64;
                                                                                                                                                                                                                                                              9.4, ITS MW IS: 44.5 kDa.
-:- SIMILARITY: WEAK, TO OTHER POLYGALACTURONASES.
Hydrolase; Glycosidase; Cell wall.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
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Bothrops jararaca (Jararaca).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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PROSITE; PS00284; SERPIN; PARTIAL.
Vasoconstrictor; Plasma; Serpin.
NON IER
SEQUENCE 8 AA: 1046 MW; DDD7611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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66.7%;
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20.0%;
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Best Local Similarity 20.0.
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Search completed: December 19, 2002, 16:44:58 Job time : 11 secs
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                              NCBI_TaxID=615;
                                                          RS10_SERMA
068936;
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-i-PTM: Rubellidin 4.2 seems to differ from Rubellidin 4.3 by its C-terminal amidation.
-i-MASS SPECTROMETRY: MW-883; METHOD=FAB.
Amphibian skin; Amidation.
MOD_RES
9
AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Steinborner ST., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
Steinborner M.J., Walled J.C.,
"The structure of new peptides from the australin red tree frog
'Litoria rubella'. The skin peptide profile as a probe for the study
of evolutionary trends of amphibians.";
Aust. J. Chem. 49:955-963(1996).
                                                                                                                                                                                                   "Purification and structure of mosact and its derivatives from the egg jelly of the sea urchin Clypeaster japonicus."; 2001. Scil. 4:649-656(1987).
-1- FUNCTION: STIMULATES SPERM RESPIRATION AND MOTILITY. PIR, JN0026; JN0026.
SEQUENCE 9 AA; 914 MW; 93245721EDC5BAB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUB=Skin secretion; Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.; Webnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.; Peptides from the skin glands of the Australian buzzing tree frog Litori electrica. Comparison with the skin peptides from Litoria.rubella.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RE42_LITRU STANDARD; PRT; 9 AA.
P82075; P82093;
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Created)
16-JUN-2002 (Rel. 41, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aust. J. Chem. 52:639-645(1999).
-!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
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                                                                                                                             TISSUE=Egg jelly;
Suzuki N., Kurita M., Yoshino K.I., Kajiura H., Nomura K.,
Yamaguchi M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.1%; Score 12; DB 1; Length 9; 66.7%; Pred. No. 1.1e+05; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                      26.1%; Score 12; DB 1; Length 9; 100.0%; Pred. No. 1.1e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
Echinoidea; Euechinoidea; Gnathostomata; Clypeasteroida;
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                          Clypeasteridae; Clypeaster
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nes 4; Conservative
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NCBI_TaxID=104895;
                                                     NCBI_TaxID=7644;
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6 HL 7
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SEQUENCE
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                                                                                                     SEQUENCE.
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RE42_LITRU
RE42_LITRU
AC P82075
DT 15-JUN
DT 15-JUN
DT 15-JUN
DE RUBEll
OC EUKACY.
OC BELOAT
OC PELOAT
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RN TYLE
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S.M., Lindahl L., Zengel J.M.;

Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: Involved in the binding of tRNA to the ribosomes (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity).
-!- SIMILARITY: BELONGS TO THE S10P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Pred. No. 1.1e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 9 AA; 1214 MW; DE3944004416D456 CRC64;
                                                                                        30-MAY-2000 (Rel. 39, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 30s ribosomal protein S10 (Fragment).
9 AA.
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InterPro; IPR001848; Ribosomal_S10.
PROSITE; PS00361; RIBOSOMAL_S10; PARTIAL.
PRT;
                                                                Created)
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Similarity 66.7%;
2; Conservative
STANDARD;
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                                                                                                                                                                                                                             Serratia marcescens
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Q9r7e8 6

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09rq49 b 09r7t2 e 09uhk1 h

09rq57

homo sapien

09udz4

099mg3 mus musculu 061723 mus musculu Q977e8 escherichia Q99887 homo sapien Q9um87 homo sapien

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09byy5 homo sapien
002831 oryctolagus
09bfc3 didelphis m
09bfc1 choloepus eu
09bfc1 choloepus d
09bf69 euphractus
09bf89 euphractus
09bf89 tamandua te
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P82445 PRELIMINARY; PRT; 7 AA.
P82445,
01-JUN-2000 (TrEMBLrel. 14, Careated)
01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
10 kDa cell wall protein (Fragment).
Nicotiana tabacum (Common tobacco).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CV. PETIT HAVANA;
Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
Woltaszek P., Bolwell G.P.;
"Proteomic study of secondary cell wall proteins from transformed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana. NCBI_TaxID=4097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 AA; 758 MW; 69D2C1E862D1B2A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SUBCELLULAR LOCATION: CELL WALL.
-1- TISSUE SPECIFICITY: XYLEM.
Cell wall.
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Planta 0:0-0(2000)
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09xnp8 boophilus m
047410 escherichia
09vw82 drosophila
008979 mus musculu
063480 rattus norv
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                                                                                             December 19, 2002, 16:39:43 ; Search time 56 Seconds (without alignments) 33.115 Million cell updates/sec
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            GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Gaps

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Score 24; DB 10; Length 7; Pred. No. 6.7e+05; 3; Mismatches 1; Indels

52.2%; 42.9%;

3; Mismatches

3; Conservative

Matches Best

1 VRIGHLY 7 | :||:: VTVGHVF 7

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Q34909 locusta mig Q8wgc7 petrolisthe Q83332 murine hepa

Q8WGC7 Q83332 P83222 Q9UQA3 Q47505

P83222 streptomyce Q9uqa3 homo sapien Q47505 escherichia

Q9umc7 homo sapien Q34909 locusta miq

09xNP8 Q47410 Q9vv82 008979 Q63480 Q9UMC7 Q34909

Result

Local Similarity

Query Match

AA.

6

PRT;

PRELIMINARY;

014277 RESULT 2 Q14277 ID Q1427 ~

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Gaps

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69D6D7273B5726F0 CRC64;
                                     37.0%; Score 17; DB 12; 75.0%; Pred. No. 6.7e+05; iive 1; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boophilus microplus (Cattle tick).
 EMBL; AJ011482; CAA09625.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12,
           927 MW;
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                                                               Conservative
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Best Local Similarity
3; Conserve
                       Query Match
Best Local Similarity
'Local 3; Conserve
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              7 AA;
                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=287;
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QACEDELTA1
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MEDLINE=94366753; PubMed=8084609;
Ceccherini I., Hofstra R., Yin L., Stulp R., Barone V., Stelwagen T.,
Bocciardi R., Mijveen H., Bolino A., Seri M., Ronchetto P., Pasini B.,
Bozzano M., Buys C., Romeo G.;
"DNA polymorphisms and conditions for SSCP analysis of the 20 exons of
the ret proto-oncogene.";
Oncogene 9:3025-3029(1994).
EMBL; Ul1532; AAC50102.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-99099045; PubMed-9882359;
Izeta A., Smerdou C., Alonso S., Penzes Z., Mendez A., Plana-Duran J.,
Enjuanes L.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-88078100; PubMed-2825819;
Rasschaert D., Gelli J., Laude H.;
"Enteric coronavirus TGFN: partial sequence of the genomic RNA its organization and expression.";
Blochimie 69:591-600(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DBC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical fusion protein.
Hypothetical fusion protein.
Virusmanisable gastroenteritis virus.
Viruses: SSRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridee; Coronavirus.
                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                  Ceccherini I., Bocciardi R., Luo Y., Pasini B., Hofstra R., Takahashi M., Romeo G.; "Exon structure and flanking intronic sequences of the human RET proto-oncogene.";
                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                                               Score 19; DB 4; Length 9; Pred. No. 6.7e+05; 1; Mismatches 2; Indels
          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
RET protein short form (Fragment).
                                                                                                                                                                                                                                                                                                                                                      9 AA; 1134 MW; 034E11A9CDD1F5B0 CRC64;
                                                                                                                                                                                                     Biochem. Biophys. Res. Commun. 196:1288-1295(1993)
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MEDLINE=94071887; PubMed=7902707;
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50.0%;
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                                                                                                   NCBI_TaxID=9606;
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"The novel mitochondrial gene arrangement of the cattle tick,
Boophilus microplus: fivefold tandem repetition of a coding region.";
Mol. Biol. Evol. 16:732-740(1999).
EMBL: AFIL0616; AAD28386.1; -.
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Parasitiformes; Ixodida; Ixodidae; Boophilus.
NCBL_TaxID=6941;
                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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STRAIN-YMC704; TRANSPOSON=CLASS I INTEGRON;
LEE K., Chong Y., Yum J.H., Yong D., Livermore D.M.;
Lee K., Chong Y., Yum J.H., Yong D., Livermore D.M.;
Nut-2 metallo-bera-lactamase gene-containing integron in a Pseudomonas aeruginosa clinical isolate.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
BMBL, AY029772; AAK50441.1; -.
NON_TER 8
093SP2;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Ouaternary ammonium compound-resistance protein QacEdeltal
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Last annotation update)
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60.0%;
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Best Local Similarity
Matches 2; Conserv
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Best Local Similarity
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NON_TER
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Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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                                               Gaps
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EMBL; X02302; CAA26166.1; -.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                        0; Indels
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32.6%; Score 15; DB 8; Length 8; 100.0%; Pred. No. 6.7e+05; Live 0; Mismatches 0; Indels
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9 Aa; 1055 MW; DCFA6412CDD1E87D CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Last annotation update)
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MEDLINE=85160860; PubMed=2580099;
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Escherichia coli.
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Quest Local Similarity 100.00
Best Local Similarity 2, Conservative
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                     Best Local Similarity 100.
Matches 3; Conservative
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NCBI_TaxID=562;
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Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

B. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B. C., Dunn P.,

R. Durbin K.J. Evangelista C.C., Ferrac C., Ferriera S., Fleischmann W.,

R. Durbin K.J. Evangelista C.C., Ferrac C., Ferriera S., Fleischmann W.,

R. Godek A., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris M.,

Harris N.L., Harrey D., Heinan T.J., Weil M.-H., Ibegwam C.,

R. Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A.,

R. Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A.,

R. Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin Z.,

R. Lu X., Mattei B., McIntosh T.C., Morris J., Moshrefi A.,

Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

R. Nelson D.K., Nison K., Nixon K., Nuskern D.R., Pacle J.M.,

R. Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Rese M.G.,

R. Shie B.C., Siden Krämos I., Simpson M., Skupski M.P., Smith T.,

Shie B.C., Siden Krämos I., Simpson M., Skupski M.P., Smith T.,

R. Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,

R. Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

R. Gibbs R.A., Wyers E.W., Rubin G.M., Venter J.C.,

R. Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.,

R. Schence Squence of Drosophila melanogaster.",

R. Schence S. Salshills S. Salston R. Smith H.O.,

R. Schence S. Salston R. Subin R., Smith H.O.,

R. Schence S. Salston R. Subin R., Shon K., Zhou K., Zhou K., Enger B., Smith H.O.,

R. Schence S. Salston R. Subin R., Shon K., Shon R., 
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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EMBL; Y11802; CAA72496.1; -.
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STRAIN=NMEI; TISSUE-MURINE RETROVIRUS INDUCED TUMOR;
STRAIN=NMEI; TISSUE-MURINE RETROVIRUS INDUCED TUMOR;
STRAIN=NMEI; TISSUE-MURINE RETROVIRUS INDUCED TUMOR;
Amtoff H.W., Sorensen A.B., Bareil C., Schmidt J., Luz A.,
Pedersen F.S.;
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Pred. No. 6.7e+05;
0; Mismatches 2;
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Query Match
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Matches 2; Conserv
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SEQUENCE
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                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                   MEDIATE-96198747: PubMed-8612486;
MEDIATE-96198747: PubMed-8612486;
Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
Detera-Wadleigh S.D.;
"Splice variants of rat TR4 orphan receptor: differential expression of novel sequences in the 5'-untranslated region and C-terminal
                                                                                                                                                                                                                                                                                                                                               Gaps
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Chave K.J., Shell K., Sanders P.G.,;
Chave K.J., Shell K., Sanders P.G.,;
Isolation and characterisation of human genomic sequences encoding cytosolic serine hydroxymethyltransferase.";
Blochem. Soc. Trans. 25:53-53(1997).
Blochem. Soc. Trans. 15:53-53(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 6.7e+05;
1; Mismatches 2; Indels
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Pred. No. 6.7e+05;
1; Mismatches 1; Indels
                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TR4-NS orphan receptor (Fragment).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                                                                                                                                                                                                                                                          NON_TER 1 1 1
SEQUENCE 7 AA; 758 MW; 672AA87864005350 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          8 AA.
                                                              PRT;
                                                                                                                                                                                                                                                           Endocrinology 137:1562-1571(1996).
EMBL; U59125; AAB02827.1; -.
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                                                                                                                                                                                                                                                                                                                        28.3%; 50.0%;
                                                                                                                                                                                                                                                                                                                                              3; Conservative
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                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHMT protein (Fragment)
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Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                  NCBI_TaxID=10116;
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2 IRGGDL 7
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_ H5
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                                                            Q63480
Q63480;
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                                                                                                                                                                                                                                                                                                                                            MEDLINE-88223478; PubMed=2836084; MEDLINE-88223478; PubMed=2836084; MCTracken A., Uhlenbusch I., Gellissen G.; Mctracken A., Uhlenbusch I., Gellissen G.; Structure of the cloned Locusta migratoria mitochondrial genome: restriction mapping and sequence of its ND-1(URF-1) gene."; Curr. Genet. 11:625-630(1987). Mitochondrion.

Mitochondrion.

NON_TER

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NON_TER

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SEQUENCE 8 AA; 1019 MW; F8E33723304845B6 CRC64;
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                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta.
NCBI_TaxID=7004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Mitochondrial gene rearrangements support a hypothesis of evolution to the crab-like form.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF436049; AAL31623.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 13; DB 8; Length 8; Pred. No. 6.7e+05; 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Bucarida; Decapoda; Plecyemata; Anomura; Galatheoidea; Porcellanidae; Petrolisthes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Morrison C.L., Harvey A.W., Lavery S., Tieu K., Huang Y.,
Cunningham C.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 13; DB 8; Length 8; Pred. No. 6.7e+05;
                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Cytochrome b (Fragment).
Locusta migratoria (Migratory locust).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
NADH dehydrogenase subunit 1 (Fragment).
Petrolisthes armatus (green porcelain crab).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 8 AB; 1010 MW; FE20504B54472696 CRC64;
8 AA.
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Similarity 20.0%;
1; Conservative
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ilarity 66.78;
Conservative
PRELIMINARY;
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RESULT 13 Q83332 ^

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-!- FUNCTION: INVOLVED IN DNA DEGRADATION IN THE SUBSTRATE MYCELIUM.

-!- FUNCTION: INVOLVED IN DNA DEGRADATION IN THE SUBSTRATE MYCELIUM.

CUTS DNA NONSPECIFICALLY. POSSESSES ENDONUCLEDLYTIC ACTIVITY.

-!- FUNCTIE REGULATION: STIMULATED BY MAGNESIUM AND MANGANESE.

INHIBITED BY ZINC AND AURIN TRICARBOXYLIC ACID.

-!- SUBCELLUAR LOCATION: SECRETED.

-!- SUBCELLUAR LOCATION: SECRETED.

MYCELIUM FORMATION AND SPORULATION.

MYCELLUM FORMATION AND SPORULATION.
                                                                                 murine hepatitis virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SECUENCE, FUNCTION, ENZYME REGULATION, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.

STRAIN=ATCC 11891;

MEDLINE=99329048; PubMed=10400660;

Micieza R.G., Huergo J., Connolly B.A., Sanchez J.;

Purification, characterization, and role of nucleases and serine proteases in Streptomyces differentiation. Analogies with the biochemical processes described in late steps of eukaryotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria, Firmicutes, Actinobacteria, Actinobacteridae,
Actinomycetales, Streptomycineae, Streptomycetaceae, Streptomyces.
NCBI_TaxID=1890;
                                                                                                                                                                         MEDLINE=95191005; PubMed=7884877;
Kim K.H., Makino S.;
"Two murine coronavirus genes suffice for viral RNA synthesis.";
J. Virol. 69:2313-2321(1995).
EMBL; U19933; AAA69002.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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0
                                                                                                                                                                                                                                                                                                                 28.3%; Score 13; DB 12; Length 8; 66.7%; Pred. No. 6.7e+05; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 28.3%; Score 13; DB 2; Length 9; Best Local Similarity 60.0%; Pred. No. 6.7e+05; Matches 3; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
34 kDa extracellular nuclease (EC 3.-.-.) (Fragment).
Streptomyces antibioticus.
                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                        8 AA; 907 MW; 92273B5B1735A2CD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 AA.
                             Created)
                         01-NOV-1996 (TrEMBLrel. 01, Created 01-NOV-1996 (TrEMBLrel. 01, Last st 01-DEC-2001 (TrEMBLrel. 19, Last ar Hemagglutinin esterase (Fragment).
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 PRELIMINARY;
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Matches 2; Conserv
                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                             NCBI_TaxID=11138;
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6 YLL 8
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SEQUENCE
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P83222
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"Two short sequences have positive effects on the human p27(Kipl) gene
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                                                                                                                                                                                                                                                                                                                                                                                                     Ito E., Iwahashi Y., Yanagisawa Y., Suzuki Y., Sugano S., Yuasa Y.,
                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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0
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                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                transcription.";
Gene 228:93-100(1999).
BMLL; AB005590; BAA76715.1; -.
NON TER
SEQUENCE 9 AA, 963 MW; 984D55A2D412C455 CRC64;
                                                                                                        9 AA.
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SEQUENCE FROM N.A.
MEDLINE-99173873; Pubmed-10072762;
                                                                                                          PRT;
                                                                                                                                                                                                              P27kipl protein (Fragment).
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                                                                                                          PRELIMINARY;
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4 VRVSN 8
  4 IGODY
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Matches
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Immunogenic peptid MAGE-2 To peptide (re MAGE-2 peptide (re MAGE-2 170 peptide MAGE-2 peptide (re Immunogenic peptide MAGE-2 peptide (re Immunogenic peptide MAGE-2 peptide MAGE-2 peptide (re Immunogenic peptide MAGE-2 HLA-B) super MAGE-170 analogue MAGE-2 170 analogue MAGE-2 170 analogue MAGE-3 nonapeptide MAGE-3 nonapeptide MAGE-3 nonapeptide MAGE-3 nonapeptide MAGE-3 nonapeptide

OM protein

Run on:

Sednence:

Searched:

Database

26 4 5 2 6 1 0 1 0 1 0 1

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Human, MACE-12; immunostimulant, gene therapy; cytostatic; immunotherapy; vaccine; melanoma; T-cell epitope; tumour rejection antigen; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel T cell epitope of MAGE-12 is a tumor rejection antigen for melanoma expressing HLA-Cw0702 recognized by tumor-infiltrating lymphocytes and useful to treat cancer particularly melanoma -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
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                                                     AAY47950
AAY48191
AAE06856
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AAG84719
AAG84726
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AAY53543
AAY45880
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AAW36555
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ABJ00185
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AAR50284
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AAR99346
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AAW54606
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 29-MAR-2001; 2001WO-US10312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAR-2000; 2000US-193206P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
 WPI; 2001-662964/76.
N-PSDB; AAD21284.
WO200174847-A2.
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 MAGE-21 nonapeptid
MAGE-21 nonapeptid
Immunogenic peptid
MAGE-A12 human leu
MAGE3 HLA-B7 super
Tumour associated
MAGE-2 170 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human MAGE-12 T-ce
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MAGE-A12 human leu
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                                                                                                          (without alignments)
21.415 Million cell updates/sec
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/ SIDS2/ggdata/geneseq/geneseqp_emb1/AA1999.DAT:*
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/ SIDS2/ggdata/geneseq/geneseqp_emb1/AA2001.DAT:*
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Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                          December 19, 2002, 16:38:38
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Maximum Match 100%
Listing first 45 summaries
                                                                 - protein search, using sw model
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AAE02084
AAR50283
AAR99345
AAR99345
AAR9446062
AAE02081
AAE02081
AAB76152
AAW45704
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46
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Match Length
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Peptide used to pr MAGE-3 protein fra MAGE-1 synthetic p Human MAGE-3 pepti Peptide 1 from Mag

Tumour antigenic p Human MAGE-3 prote Immunogenic peptid

Melanoma antigen ( MAGE 3 immunogenic MAGE-3 nonapeptide

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RESULT 3
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                                                                                               infiltrating lymphocytes. The epitope or a vector encoding the epitope is used to treat cancer, particularly melanoma expressing HLA-CW staterisk 0702. The epitope has widespread utility in cancer immunotherapy since MAGE-12 is mostly found in tumours. The present sequence is human MAGE-12 T-cell epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The patent discloses antigenic peptides derived from MAGE-A12 protein and presented by human leukocyte antigens (HLAs). These antigenic peptides when presented by an antigen presenting cell having a HLA class I molecule, effectively induce the activation and proliferation of CD8+ cytotoxic T lymphocytes. MAGE-A12 is useful for treating a subject having a disorder characterised by expression of MAGE-A12. The protein microarray comprising MAGE-A12 is useful for diagnosing a disorder, especially cancer, by determining the binding of an antibody, T lymphocytes or a HLA molecule isolated from the subject suspected of having the disorder characterised by the expression of MAGE-A12. MGE-A12 is useful for treating cancers, including bladder carcinomas, melanomas, oesophageal, lung, head and neck, ibreast, colorectal carcinomas, myelomas, brain tumours, sarcomas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antigenic peptides derived from MAGE-A12 polypeptides, useful for diagnosis and treatment of cancer, such as bladder, lung, breast, brain, prostate and renal carcinomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cytostatic; immunogen; MAGE-A12; human leukocyte antigen; HLA; CD8; cytotoxic T lymphocyte; cancer; carcinoma; melanoma; myeloma; brain tumour; sarcoma; vaccine; gene therapy.
                                                                                                                                                                                                                                                                                    Gaps
                                               The invention relates to an isolated and purified T cell epitope candGE-12. MAGE-12 is a tumour rejection antigen for melanoma which expresses MHC-class I molecule HLA-Cw0702 recognised by tumour-
                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                               Length 9;
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                                                                                                                                                                                                                                                                                Indels
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0
                                                                                                                                                                                                                                               Score 46; DB 22;
Pred. No. 7.8e+05;
                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE02082 standard; peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Page 42; 69pp; English.
                Claim 1; Page 14; 17pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Van Den Eynde B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                               100.0%;
100.0%;
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2000US-0179570.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                    9; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                Sequence
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The patent discloses antigenic peptides derived from MAGE-A12

protein and presented by human leukocyte antigens (HLAs). These
antigenic peptides when presented by an antigen (HLAs). These
antigenic peptides when presented by an antigen presenting cell
having a HLA class I molecule, effectively induce the activation
and proliferation of CD8+ cytocxic T lymphocytes. MAGE-A12 is
useful for treating a subject having a disorder characterised by
expression of MAGE-A12. The protein microarray comprising MAGE-A12
is useful for diagnosing a disorder, especially cancer, by determining
the binding of an antibody, T lymphocytes or a HLA molecule isolated
from the subject suspected of having the disorder characterised by the
cxpression of MAGE-A12. MAGE-A12 is useful for treating cancers,
including bladder carcinomas, melanomas, oesophageal, lung, head and
neck, breast, colorectal carcinomas, myelomas, brain tumours, sarcomas,
prostate and renal carcinomas and to produce antibodies. MAGE-A12
antibodies are useful for diagnosing disorders characterised by
cexpression of MAGE-A12 immunogenic polypeptide. These MAGE-12 peptides
are used as vaccines. They are also used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
prostate and renal carcinomas and to produce antibodies. MACE-Al2 antibodies are useful for diagnosing disorders characterised by expression of MACE-Al2 immunogenic polypeptide. These MAGE-12 peptides are used as vaccines. They are also used in gene therapy. The present sequence is MAGE-Al2 HLA class I-binding peptide. This antigenic peptide is presented by major histocompatibility complex (MHC) and is recognised by CTLs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antigenic peptides derived from MAGE-A12 polypeptides, useful for diagnosis and treatment of cancer, such as bladder, lung, breast, brain, prostate and renal carcinomas -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cytostatic; immunogen; MAGE-Al2; human leukocyte antigen; HLA; CD8; cytotoxic T lymphocyte; cancer; carcinoma; melanoma; myeloma; brain tumour; sarcoma; vaccine; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                    Length 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAGE-A12 human leukocyte antigen-binding peptide #4.
                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 46; DB 22;
100.0%; Pred. No. 7.8e+05;
1ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Van Den Eynde B, Boon-Falleur T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE02084 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 43; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-OCT-2000; 2000WO-US28852.
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01-FEB-2000; 2000US-0179570.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                    9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                                                                                        Sequence
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AAR99345 standard; Protein; 9 AA.
                                                                                                                                                                       22-APR-1997 (first entry)
                                                                                                                                                                                                                 MAGE-21 nonapeptide.
                                                                                                                                  AAR99345;
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                                                  RESULT 5
AAR99345
                                                                                           NAME OF THE PROOF 
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                                                                                                                                                                       Gaps
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The present sequence is MAGE-A12 HLA class-I-binding peptide. This antigenic peptide is presented by major histocompatibility complex (MHC) and is recognised by CTLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nona:peptide derived from tumour rejection antigen precursor - presented by HLA-Al cancer cells, for use in diagnosis or therapy of esp. melanoma and breast cancer.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAGE; nonapeptide; cancer; melanoma; breast cancer; HLA; histocompatability; human leucocyte antigen; probe; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.6%; Score 38; DB 15; Length 9; 100.0%; Pred. No. 7.8e+05; rive 0; Mismatches 0; Indels
                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Traversari C;
                                                                                                                            Score 42; DB 22; Pred. No. 7.8e+05;
                                                                                                             91.3%; Sco.
100.0%; Pred. No. '...
'... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 20; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                        AAR50283 standard; Protein; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92US-0938334.
93US-0037230.
93US-0073103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93WO-US08157.
                                                                                                                                                                                                                                                                                                                                                                                                                                       26-SEP-1994 (first entry)
                                                                                                                          Query Match 91.3'
Best Local Similarity 100.'
Matches 8; Conservative
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Best Local Similarity 100.0
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAGE-21 nonapeptide.
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Van Derbruggen P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAQ44753.
                                                                                  8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapy; vaccine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 AA;
                                                                                                                                                                                                          2 RIGHLYIL 9
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26-MAR-1993;
07-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9405304-A.
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                                                                                     Sequence
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AAR50283
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AAR99343-R99350 represent MAGE nonapeptides, based on the tumour rejection antigen region of the full length MAGE sequences. These peptides were used to design the nonapeptides of the invention (see AAR9933-R99342), which bind to a HLA molecule on a cell, and provoke. Iysis by cytolytic T cells (CTLS) specific for a complex of the HLA molecule and nonapeptide. The nonapeptides can be used diagnostically to identify tumours expressing a particular HLA molecule, or to identify cancer cells. The peptides can also be used therapeutically, to induce a CTL response to tumours (where the peptides are optionally coupled to tumour specific antibodies), or to induce a response by CTLs that are cotherwise inactive. The peptide sequences may also be used to expand the peptides are return to the patient, such as for treating melanoma. Tumour cells can be identified by using DNA encoding the nonapeptides as probes. Non-human cells transformed with the HLA-Al congenerate CTLs, or to detect the presence of CTLs in human samples. The non-human transformed cells, when polytransformed, are universal effector cells.
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HLA binding peptide; cell lysis; cytolytic T cell; MAGE family; human; tumour rejection antigen precursor; TRA; MAGE-1; tumour; cancer cell; antibody; melanoma; universal effector cell; vaccine; breast cancer; CTL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nona:peptide(s) that bind to HLA molecule(s) and induce lysis by specific cytolytic T cells, for diagnosis and treatment of tumours and to expand T cells in vitro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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Van Der Bruggen P;
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Romero P, Traversari C, Van Den Eynde B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4; Fig 4; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-0393273.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1996-402317/40.
N-PSDB; AAT35410.
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                          WO9626214-A1
                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-FEB-1995;
                                                                                                                                                                                                                                                                                                                  29-AUG-1996.
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AAY46062

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The patent discloses antigenic peptides derived from MAGE-A12 protein and presented by human leukocyte antigens (HLAS). These antigenic peptides when presented by an antigen presenting cell having a HLA class I molecule, effectively induce the activation and proliferation of CD8+ cytotoxic T lymphocytes. MAGE-A12 is useful for treating a subject having a disorder characterised by expression of MAGE-A12. The protein microarray comprising MAGE-A12 is useful for diagnosing a disorder, especially cancer, by determining the binding of an antibody. T lymphocytes or a HLA molecule isolated from the subject suspected of having the disorder characterised by the expression of MAGE-A12 is useful for treating cancers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               including bladder carcinomas, melanomas, oesophageal, lung, head and neck, breast, colorectal carcinomas, myelomas, brain tumours, sarcomas, prostate and renal carcinomas and to produce antibodies. WAGE-Al2 antibodies are useful for diagnosing disorders characterised by expression of MAGE-Al2 immunogenic polypeptide. These MAGE-12 peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antigenic peptides derived from MAGE-A12 polypeptides, useful for diagnosis and treatment of cancer, such as bladder, lung, breast, brain, prostate and renal carcinomas
                                                                                                                                                                   Human; cytostatic; immunogen; MAGE-A12; human leukocyte antigen; HLA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              are used as vaccines. They are also used in gene therapy. The present sequence is MAGE-Al2 HLA class-I-binding peptide. This antigenic peptide is presented by major histocompatibility complex
                                                                                                                                                                                             CD8; cytotoxic T lymphocyte; cancer; carcinoma; melanoma; myeloma;
brain tumour; sarcoma; vaccine; gene therapy.
                                                                                                                    MAGE-A12 human leukocyte antigen-binding peptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82.6%; Score 38; DB 22; I
100.0%; Pred. No. 7.8e+05;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Van Den Eynde B, Boon-Falleur T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 42; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG84743 standard; Peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MHC) and is recognised by CTLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-OCT-1999; 99US-0160374.
01-FEB-2000; 2000US-0179570.
                                                                                                                                                                                                                                                                                                                                                                                                                         19-OCT-2000; 2000WO-US28852.
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                                                                   31-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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nes 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-328498/34.
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                                                                                                                                                                                                                                                                                                                      WO200129220-A2
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                                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                       26-APR-2001
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                       AAE02081;
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δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY4590 to AAY48214 represent specifically claimed immunogenic peptides having a human major histocompatibility complex (MHC) Class I (also known as human leukocyte antigen (HLA) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes (HLA-A2.1, Al, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived. Cytotoxic T lymphocytes (CTLS) which destroy antigen bearing cells are normally induced by an antigen in the form of a peptide fragment bound are particularly important in themour rejection antigen itself, and are particularly important in themour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat. Or prevent viral infections and cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or useful diagnostically, and can be used to induce a cytotoxic T cell response, by contacting a cytotoxic T cell with the peptide e.g. to produce CTLS ex vivo for infusion back into a patient. The procure is manifested as read to induce a special contacting a cytotoxic T cell with the peptide e.g. to produce CTLS ex vivo for infusion back into a patient. The
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                                                                                                                                                                     Immunogenic peptide having a human leukocyte antigen binding motif #673.
                                                                                                                                                                                                                    Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tunnor rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 20; Length 9; 7.8e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.6%; Score 38; 100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 54; 150pp; English.
                       AAY46062 standard; Peptide; 9 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98WO-US05039.
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                                                                                                                         (first entry)
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                           vaccine; immunisation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kubo RT,
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                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                       01-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                          Synthetic
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RESULT 7 AAE02081 ID AAE(

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Length 9; 0; Indels

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The present invention describes a composition (1) which comprises at least one human leukocyte antigen (HLA) binding peptide comprising an isolated, prepared epitope comprising one of 547 8-11 residue amino acid sequences (S1), given in AAB75803 to AAB7649. (1) has cytostatic, hepatotropic, antiinflammatory, anti-HIV (human immodeficiency virus) and protozoacide activities, which can be used in vaccine production and is an inducer of cytotoxic T-cell response. (1) is useful for inducing a cytotoxic T cell response against in stocompatibility complex (MHC) class I allele, by contacting cytotoxic T cells (CTLS) from the patient with (I). (I) is useful as a vaccine to treat and/or prevent viral infection and cancer such as prostate cancer, hepatitis B, hepatitis C, human papilloma virus (HPV) infection, cytomegalovirus (CMV), acquired immunodeficiency syndrome (AIDS), renal carcinoma, cervical carcinoma, lymphoma, malaria, and condyloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HLA molecule; cytotoxic T cell; immunogenic peptide; binding affinity;
HLA-B7 supermotif; tumour; infection; parasite; CTL; antigen; melanoma;
   HLA binding peptide; immune response; glycoprotein; cytostatic; virucide; hepatotropic; antiinflammatory; anti-HIV; vaccine; human immunodeficiency virus; protozoacide; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; human papilloma virus; HPV; cytomegalovirus; CMV; acquired immunodeficiency syndrome; AIDS; renal carcinoma; cervical carcinoma; lymphoma; malaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Composition comprising human leukocyte antigen binding peptide which comprises isolated, prepared epitope useful for treating viral infections such as acquired immunodeficiency syndrome, and cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAGE-2 170 peptide with binding affinity for HLA-B7-like molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 35; DB 22; L
Pred. No. 7.8e+05;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                               Southwood
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85.7%;
                                                                                                                                                                                                                                                      28-JUN-2000; 2000WO-US17842.
                                                                                                                                                                                                                                                                                         99US-0141422.
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                                                                                                              condyloma acuminatum
                                                                                                                                                                                                                                                                                                                            (EPIM-) EPIMMUNE INC
                                                                                                                                                                                                                                                                                                                                                              Sidney J,
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-112389/12.
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Best Local Similarity
Matches 6; Conserv
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IGHLYII
                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                         29-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW45704;
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                                                                                                                                                                                                                                                                                                                                                              Sette A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes MAGE2/3 epitopes (I). Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is cultured in vivo and bluds to a complex of (I); (2) a peptide (II) comprising (I) and a second epitope and has less than 50 contiguous amino acids; (3) a vaccine composition comprising (II), a unit dose of a peptide with at least 50 contiguous amino acids with 100% identity to the native peptide sequence of MAGE2/3, and a pharmacentical excipient; (4) an isolated nucleic acid encoding (II). (I) has cyclostatic activity, and can be used in vaccines and as an immunostimulant. A vaccine of (3) is useful for the treatment and immunostimulant. A vaccine of (3) is useful for the treatment and immunostimulant. A vaccine of (3) is useful for which circumpass ample from a patient with (I) that binds to an human leukocyte antipen (HLA) allele present in the patient and detecting the presence of the T-lymphocyte that binds to the petind. The vaccine allows the opportunity to combine epitopes derived from multiple tumour-associated molecules reducing the likelihood of tumour escape due to antigen loss. AAG84515 to AAG84909 and AAB99725 crepresent amino acid sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                           An isolated prepared MAGE2/3 epitope (I) for use in pharmaceuticals for the treatment and prevention of cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human leukocyte antigen; HLA; major histocompatibility complex; MHC; cytotoxic T lymphocyte; CTL; human class I MHC; immunogenic;
                                                       cytotoxic T lymphocyte;
                                               Human; human leukocyte antigen; HLA epitope; cytotoxic T lymphocyte
CTL; MAGE2; MAGE3; melanoma antigen gene; immune response; vaccine;
cancer; cytostatic; immunostimulant.
                                                                                                                                                                                                                                                                                                                                                              Celis E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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85.7%; Pred. No. 7.8e+05;
....matches 0; Indels
                                                                                                                                                                                                                                                                                                                                                            Chesnut R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumour associated antigen MAGE3 immunogenic peptide.
                                                                                                                                                                                                                                                                                                                                                          Southwood S,
                MAGE3 HLA-B7 supermotif-bearing peptide #9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 156; 171pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB76152 standard; Peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                          Sidney J,
                                                                                                                                                                                                                                               11-DEC-2000; 2000WO-US33545.
                                                                                                                                                                                                                                                                                    99US-0458298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                     (EPIM-) EPIMMUNE INC
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-375002/39.
                                                                                                                                                                                                                                                                                                                                                          Sette A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 AA;
                                                                                                                                                                         WO200142267-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 IGHLYIL 9
                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                  10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 IGHLYII
                                                                                                                                                                                                            14-JUN-2001
                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                      Fikes J,
Keogh E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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Gaps

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Length 9; Indels ဖ

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Homo sapiens
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                                        13-MAR-1998;
                                                                       13-MAR-1998;
            16-SEP-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY46263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY46263
δλ
                                                                                                                                                                                                                                                                                                                     This sequence represents an immunogenic peptide with binding affinity for HLA-B7-like molecules. A cytotoxic T cell (CTL) response against a particul ar antigen (Ag) is induced in a patient by contacting a CTL with can immunogenic peptide of 9-15 amino acids which binds to at least two an immunogenic peptide of 9-15 amino acids which binds to at least two canderes a cytotoxic T cell response. The immunogenic peptide has a compension of 9 amino acids, comprising a binding motif, with from the condernal primary anchor sites (PAR) at positions 2 (selected from Ala, Leu, Ile, Val, Met, Ser or Thr) and 9 (Arg or Lys) and at least one secondary anchor sites (SAR), i.e. Tyr, Phe or Trp at positions 3, 6 or condernal and therapeutic compositions, for treating viral, pased vaccines and therapeutic compositions, for treating viral, pased vaccines and therapeutic compositions, for treating viral, cor fungal diseases or cancer, e.g. prostatic cancer, hepatitis or condyloma acuminatum. They can also be used to elicit a CTL response or voint viral does not respond to peptide vaccines or other therapies. Che patient does not respond to peptide vaccines or other therapies. Che patient does not respond to peptide vaccines or other therapies. Che patient adminishment in thigher binding condernal cancer of affinity and thus increased immunogenicity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                    Inducing cytotoxic T cell response against specific antigen - using immunogenic peptide with binding affinity for HLA-A3-like molecules, to treat or prevent tumours and infections by virus, parasites etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.7%; Score 33; DB 18; Length 9; 77.8%; Pred. No. 7.80+05; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                               Example 2; Page 51; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY46232 standard; Peptide; 9 AA.
                                                                                                                                                                             Sidney J;
                                                                                     97WO-US03778
                                                                                                                  96US-0013113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 7/...
7: Conservative
                                                                                                                                                                              Sette A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine; immunisation.
                                                                                                                                                                                                          WPI; 1997-470637/43.
                                                                                                                                               (CYTE-) CYTEL CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 AA;
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                                                                                                                                                                             Chestnut RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
 Homo sapiens
                           WO9733602-A1
                                                                                      10-MAR-1997;
                                                                                                                  11-MAR-1996;
                                                         18-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY46232;
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ANY45390 to AAY48214 represent specifically claimed immunogenic peptides having a human major histocompatibility complex (MHC) Class I (also known as human newocyte antigen (HLA)) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes (HLA-A2.1, Al, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived.

Cytotoxic T lymphocytes (CTLS) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound are particularly important in the intact foreign antigen itself, and are particularly important in the intact foreign antigen itself, and are particularly important in the intact foreign antigen itself, or prevent viral infections and cancers in mammals (especially to treat or prevent viral infections and cancers in mammals (especially bummans) e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell response, by contacting a cytotoxic T cell with the peptide e.g. to produce CTLS ex vivo for infusion back into a patient. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunogenic peptide having a human leukocyte antigen binding motif #874.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                        New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases {\ }^{-}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                        Southwood S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.7%; Score 33; DB 20; Length 9; 77.8%; Pred. No. 7.8e+05; Live 0; Mismatches 2; Indels
                                                                                                                                                                                        Grey HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               therapeutically and for immunisation as above.
                                                                                                                                                                                        Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY46263 standard; Peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 62; 150pp; English.
                                                                                                                                                                                        Sette A, Kubo RT, Sidney J,
98WO-US05039
                                                               98WO-US05039
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                                                                                                                            (EPIM-) EPIMMUNE INC
                                                                                                                                                                                                                                                  WPI; 1999-551214/46.
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es 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 AA;
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3 IGHLYI 8
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                                                                 Sette A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY47944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY45390 to AAY48214 represent specifically claimed immunogenic peptides having a human major histocompatibility complex (MHC) Class I (also known as human leukcoyte antigen (HLA) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes ILA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived. Cytotoxic T lymphocytes (CTLS) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound are particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat or particularly important in tumour rejection and in fighting viral infections and cancers in mammals (especially humans) or prevent viral infections and cancers in mammals (especially humans) or prevent viral infections as a vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or individuals susceptible or otherwise at risk of viral infection or useful diagnostically, and can be used to induce a cytotoxic T cell response, by contacting a cytotoxic T cell with the peptide e.g. to produce CTLs ex vivo for infusion back into a patient. The polynuclectides encoding the immunogenic peptides are also useful therapeutically and for immunisation as above.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                         New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                        Southwood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.7%; Score 33; DB 20; Length 9; 100.0%; Pred. No. 7.8e+05; ive 0; Mismatches 0; Indels
                                                                                        Grey HM,
                                                                                      Sette A, Kubo RT, Sidney J, Celis E,
                                                                                                                                                                             Claim 1; Page 64; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY47329 standard; Peptide; 9 AA.
          98WO-US05039
                                    98WO-US05039
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                                                             (EPIM-) EPIMMUNE INC
                                                                                                               WPI; 1999-551214/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 IGHLYI 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 IGHLYI 8
         13-MAR-1998;
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                                    13-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY47329;
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Cytotoxic T lymphocytes (Tits) which destroy antigen bearing cells are normally induced by an antigen in the form of a peptide fragment bound to a HiA molecule, rather than the infact foreign antigen itself, and are particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) or prevent viral infections and cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cyctoxic T cell response, by contacting a cyctoxic T cell with the peptide e.g. to produce CILS ex vivo for infusion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful therapeutically and for immunisation as above.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY45390 to AAY48214 represent specifically claimed immunogenic peptides having a human major histocompatibility complex (MHC) class I (also having a human leukocyte antigen (HLA)) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived.
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                                                                                                                                                                                                                                                                                                                                                           New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases
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                                                                                                                                                                                  Southwood S;
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                                                                                                                                                                                  Grey HM,
                                                                                                                                                                             Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 103; 150pp; English.
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                                                                                                                                                                             Kubo RT, Sidney J,
98WO-US05039
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                                                                                    (EPIM-) EPIMMUNE INC
                                                                                                                                                                                                                                                                 WPI; 1999-551214/46
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Southwood

Grey HM,

Celis E,

Sidney J,

Kubo RT,

Sette A,

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                                                                                                                                                                          AAY45390 to AAY48214 represent specifically claimed immunogenic peptides having a human major histocompatibility complex (MHC) class I (also known as human leukocyte antigen (HLA) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-AZ.1, A1, A3.2 or A24.10° HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived. Cytotoxic I lymphocytes (CTLS) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen itself, and are particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunogenic peptide having a human leukocyte antigen binding motif #2561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cance prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                        They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell response, by contacting a cytotoxic T cell with the peptide e.g. to produce CILs ex vivo for infusion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful
                                                                                                    New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases \dot{}
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                                           Southwood S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 33; DB 20; Length 9;
Pred. No. 7.8e+05;
0; Mismatches 2; Indels
                                           Sidney J, Celis E, Grey HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapeutically and for immunisation as above.
                                                                                                                                                   Claim 1; Page 128; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY47950 standard; Peptide; 9 AA.
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77.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vaccine; immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EPIM*) EPIMMUNE INC.
              (EPIM-) EPIMMUNE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
7; Conserve
                                                                      WPI; 1999-551214/46.
                                           Kubo RT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-MAR-1998;
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                                           Sette A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY47950;
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having a human major histocompatibility complex (MHC) class I (also known as human leukocyte antigen (HLA) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived. Cytotoxic T lymphocytes (CTLS) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen itself, and are particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell response, by contacting a cytotoxic T cell with the peptide e.g. to produce CTLS ex vivo for infusion back into a patient. The
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                                                                                                                                                                                                                                                                                                AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
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                                                                                 New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polynucleotides encoding the immunogenic peptides are also useful therapeutically and for immunisation as above.
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Job time : 64 secs
                                                                                                                                                                                                               Claim 1; Page 129; 150pp; English.
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Best Local Similarity
6; Conserve
WPI; 1999-551214/46.
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3 IGHLYI 8
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us-09-692-401-4.closed.rapb

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December 19, 2002, 16:45:03; Search time 11 Seconds (without alignments) 13.716 Million cell updates/sec
GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                        106657 segs, 16763532 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                     OM protein - protein search, using sw model
                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                     US-09-692-401-4
46
1 VRIGHLYIL 9
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                                                                                                                                                                                     Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                           Run on:
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// Cont.\_6/ptodata/2/pubpaa/USOB\_NEW\_PUB.pep:\*
/ Cgn2\_6/ptodata/2/pubpaa/USOB\_NEW\_PUB.pep:\*
/ Cgn2\_6/ptodata/2/pubpaa/USOB\_NEW\_PUB.pep:\*
/ Cgn2\_6/ptodata/2/pubpaa/USOG\_NEW\_PUB.pep:\*
/ Cgn2\_6/ptodata/2/pubpaa/USOG\_NEW\_PUB.pep:\*
/ Cgn2\_6/ptodata/2/pubpaa/USOB\_NEW\_PUB.pep:\*
/ Cgn2\_6/ptodata/2/pubpaa/USOB\_NEW\_PUB.pep:\*
/ Cgn2\_6/ptodata/2/pubpaa/USOB\_NEW\_PUB.pep:\*
/ Cgn2\_6/ptodata/2/pubpaa/USOB\_USEW\_PUB.pep:\*
/ Cgn2\_6/ptodata/2/pubpaa/USOB\_USEW\_PUB.pep:\*
/ Cgn2\_6/ptodata/2/pubpaa/USOB\_USEW\_PUB.pep:\*
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/ Cgn2\_6/ptodata/2/pubpaa/USOB\_USUBCOMB.pep:\*
/ Cgn2\_6/ptodata/2/pubpaa/USOB\_USUBCOMB.pep:\*
/ Cgn2\_6/ptodata/2/pubpaa/USOB\_USUBCOMB.pep:\*
/ Cgn2\_6/ptodata/2/pubpaa/USOB\_USUBCOMB.pep:\* Published\_Applications\_AA:\* ••

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 58. Appl	Sequence 30, Appl	67.	Sequence 31, Appl	Sequence 100, App	Sequence 18, Appl	Sequence 56, Appl	51.	i m	23.	. ~		V	Sequence 3, Appli		Sequence 24. Appl	Segmence 95. April	Sequence 38. Appl	Sequence 538, App	,
qı	US-09-766-889A-58	US-09-017-743C-30	US-09-017-743C-67	US-09-017-743C-31	US-09-017-743C-100	US-09-766-889A-18	US-09-766-889A-56	US-09-909-460-51	US-09-812-528-3	) US-09-847-185-23	US-09-923-831-6	US-09-017-743C-32	US-09-766-889A-7	: US-10-026-001-3	US-09-894-018-319	US-09-826-290-24	US-09-826-290-95	US-09-017-743C-38	US-09-791-378-538	
% Query Match Length DB	7 9 9	7 9 9	7 9 9	4 9 9	6 8 0	6 6 0	6 6 0	6 6 0	0 9 10	0 9 10	0 9 10	6 6 6	5 9 9	5 9 12	2 9 10	6 6	6 6 0	6 6 0	0 9 10	
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Score	33	33	33	31	52	52	58	52	57	25	56	28	26	26	24	23	23	23	23	
Result No.	П	7	æ	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	

APPLICANT: Sette, Alessandro

Sequence 79, Appli Sequence 1, Appli Sequence 16, Appli Sequence 17, Appli Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 16, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl	BIND HLA-B35 AND HLA-B44	Length 9; ; Indels 0; Gaps 0;
7 10 US-09-765-086-79 7 10 US-09-765-801-1 8 10 US-09-766-875-16 8 10 US-09-756-875-17 9 10 US-09-756-875-17 9 10 US-09-756-983-6-9 10 US-09-756-983-6-9 10 US-09-756-983-123-9 10 US-09-813-718-42 7 9 US-10-801-123-85-123-9 7 10 US-09-813-718-12 7 10 US-09-813-718-10 8 9 US-10-801-187-10-10 8 9 US-09-911-878-10-10 8 9 US-09-766-889A-10 8 9 US-09-766-889A-10 9 US-09-80-460-91 9 US-09-80-460-91	ALIGNMENTS  989A  IC PEPTIDES WHICH 177,242 243,212 243,212 FSION 3.0	33; DB 9; . No. 8.9e+04 smatches 0
20 22 47.8 21 22. 23 21 45.7 25.7 25.7 25.7 25.7 26.7 26.7 26.7 27.8 31.3 32.3 31.3 32.3 32.3 34.3 35.5 35.5 35.5 35.5 35.5 35.5 35	RESULT 1  US-09-766-889A-58  Sequence 58, Application US/09766  Patent No. US:0020164654A1  GENERAL INFORMATION: APPLICANT: LOITEN, Rosalie APPLICANT: Wan der Bruggen, Ple- APPLICANT: Stroobant, Vincent APPLICANT: Stroobant, Vincent APPLICANT: Schultz, Ervin TITLE OF INVENTION: MadE ANTIGEN FILE REFERENCE: LO461/7104 CURRENT APPLICATION NUMBER: US/OF CORRENT FILING DATE: 2001-01-19 FRIOR APPLICATION NUMBER: US 60/PRIOR FILING DATE: 2000-10-25 NUMBER OF SEQ ID NOS: 59  SOFTWARE: FastSEQ for Windows Ve: SEQ ID NO 58  LENGTH: 9  TYPE: PRT  COGGANISM: Homo sapiens	Query Match Best Local Similarity 100.0%; Pred Matches 6; Conservative 0; Mi, QY 3 IGHLYI 8                 Db 3 IGHLYI 8   SCULT 2   US-09-017-743C-30   Sequence 30, Application US/09017743C   Patent No. US20020177694A1   GENERAL INFORMATION:

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Score 33; DB 9; Length 9;
Pred. No. 8.9e+04;
0; Mismatches 2; Indels
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ADDRESSEE: Twomsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sidney, John Southwood, Scott INVENTION: HLA Binding Peptides and Their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUBER: US/09/017,743C
FILING DATE: 03 Feb-1998
CLASSIFICATION: <Unknown>
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 018623-008050US
                                                                                                                               APPLICATION NUMBER: US 08/590,298
FILING DATE: 23-JAN-1996
ATTORNEX/AGENT INFORMATION:
NAME: PARENT, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 018623-008050US
                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/017,743C
FILING DATE: 03-Feb-1998
CLASSIFICATION: <UNKNOWN>
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APPLICATION NUMBER: US 08/590,298
FILING DATE: 23.3AN-1996
ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-017-743C-67
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TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
TELEX: CURROWN
                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                             TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Sette, Alessandro
                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.78;
77.88;
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                                                                                                                 PRIOR APPLICATION DATA:
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Best Local Similarity 77.8
Matches 7; Conservative
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ZIP: 94111-3834
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US-09-017-743C-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sidney, John Southwood, Scott TITLE OF INVENTION: HLA Binding Peptides and Their USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 146
CORRESPONDENCE ADDRESS:
ANDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
  Sidney, John
Southwood, Scott
TITLE OF INVENTION: HLA Binding Peptides and Their
                                                                                                                               ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                              CURRENT TIPE: LISANCIAE
COMBUTER: IBM Compatible
COMBUTER: IBM Compatible
COPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/017,743C
FILING DATE: 03-Feb-1998
CLASSIFTCATION NUMBER: US 08/590,298
FILING DATE: 23-JAN-1996
ATTORREY/AGENT INFORMATION:
NAME: PARENT, ANNELTE S.
RECISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 018623-008050US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHANGE: 415-576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-017-743C-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONVERT: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 67, Application US/09017743C Patent No. US20020177694A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Sette, Alessandro
                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
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                                                                                            NUMBER OF SEQUENCES: 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
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                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: <Unknown>
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Matches 7; Conservative
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0; Gaps

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APPLICANT: Luiten, Rosalie
APPLICANT: Luiten, Thierry
APPLICANT: Luiten, Thierry
APPLICANT: Boon-Falleur, Thierry
APPLICANT: Stroobant, Vincent
APPLICANT: Stroobant, Vincent
APPLICANT: Stroobant, Vincent
APPLICANT: Schultz, Erwin
TILE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44
CURRENT APPLICATION NUMBER: US/09/766,889A
CURRENT FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 60/17,242
PRIOR APPLICATION NUMBER: US 60/17,242
PRIOR APPLICATION NUMBER: US 60/243,212
PRIOR FILING DATE: 2000-10-25
PRIOR PILING DATE: 2000-10-25
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 18
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Stroobant, Vincent
APPLICANT: Stroobant, Vincent
APPLICANT: Stroobant, Vincent
APPLICANT: Demotte, Nathalie
APPLICANT: Demotte, Nathalie
APPLICANT: Demotte, Nathalie
TITLE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44
FILE REFERENCE: L0461/7104
CURRENT APPLICATION NUMBER: US/09/766,889A
CURRENT APPLICATION NUMBER: US 60/177,242
PRIOR APPLICATION NUMBER: US 60/177,242
PRIOR APPLICATION NUMBER: US 60/243,212
PRIOR FILING DATE: 2000-10-25
PRIOR FILING DATE: 2000-10-25
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.0%; Score 29; DB 9; L
100.0%; Pred. No. 8.9e+04;
tive 0; Mismatches 0;
                                                                                                                 ; Sequence 18, Application US/09766889A
; Patent No. US20020164654A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 56, Application US/09766889A Patent No. US20020164654A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Luiten, Rosalie
APPLICANT: Boon-Falleur, Thierry
APPLICANT: van der Bruggen, Pierre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.00,
100.0%; Pre-
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; ORGANISM: Homo sapiens
US-09-766-889A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 5; Conserv
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Matches 5; Conserv
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             1 VPISHLYI
                                                                     RESULT 6
US-09-766-889A-18
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5 IGHLY 9
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| IGHLY 9
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                                                                                                                                                                                                                  Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Sette, ....
Sidney, John
Southwood, Scott
FITLE OF INVENTION: HAS Binding Peptides and Their
Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: CA
COUNTRY: USA
ZIP: 94111-3984
ZIP: 94111-3984
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASLSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/017,743C
FILING DATE: 03-Feb-1998
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/590,298
FILING DATE: 23-JAN-1996
ATORNEY/AGENT INFORMATION:
NAME: Parent, Annete S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 018623-008050US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0300
TELEX: 415-576-0300
                                                                                                                                                                                                              DB 9; I
8.9e+04;
                                                                                                                                                                                                              Score 31; DB Pred. No. 8.9e-0; Mismatches
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-09-017-743C-100
                                                                                                        ; TOPOLOGY: linear

; MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 31:

US-09-017-743C-31
                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
US-09-017-743C-100
; Sequence 100, Application US/09017743C
; Patent No. US20020177694A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                       0;
                                         LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 100: SEQUENCE CHARACTERISTICS:
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                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
INFORMATION FOR SEQ ID NO: 31:
                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                              67.4%;
85.7%;
                                                               TYPE: amino acid
                                                                                                                                                                                                            Query Match 67.4
Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity
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3 ISHLYIL 9
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TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
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| IGHLY 9
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                                                                                                                                    APPLICANT: LUNSford, Lynn B.
APPLICANT: Putnam, David
APPLICANT: Putnam, David
APPLICANT: Hedley, Mary Lynn
TITLE OF INVENTION: MCROPARTICLES FOR DELIVERY OF NUCLEIC
TITLE OF INVENTION: ACID
FILE REPERENCE: 0819/1/014001
CURRENT APPLICATION NUMBER: US/09/909, 460
CURRENT APPLICATION NUMBER: EARLIER PELICATION NUMBER: US/09/321, 346
PRIOR FILING DATE: BARLIER FILING DATE: 1999-05-27
NUMBER OF SEQ ID NOS: 114
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 51
LENGTH: 9
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GENERAL INCORMATION:
APPLICANT: Walliam
APPLICANT: Walliam
APPLICANT: Walliam
TILE OF INVENTION: STRUULATION OF HEMATOPOIETIC CELLS IN
TILLE OF INVENTION: VITRO
FILE REFERENCE: 10248/7015
CURRENT APPLICATION NUMBER: US/09/812,528
CURRENT FILING DATE: 2001-03-20
PRIOR FILING DATE: 1997-09-29
PRIOR PRILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 9
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Patent No. US20020076392A1
GENERAL INFORMATION:
APPLICANT: SOO HOO, William
                                                                            Sequence 51, Application US/09909460 Publication No. US20020182258A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09812528 Patent No. US20010018210A1
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Best Local Similarity 10v.v
5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT; ORGANISM: Homo sapiens
US-09-909-460-51
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IGHLY 9
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5 IGHLY 9
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US-09-847-185-23
                                                         US-09-909-460-51
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COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE RESPONSE USING SAME
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APPLICANT: Martelange, Val, rie
APPLICANT: De Smet, Charles
APPLICANT: De Son-Falleur, Thierry
TITLE OF INVENTION: TUMON ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR
FILE REFERENCE: L0461/7054
CURRENT APPLICATION NUMBER: US/09/923,831
CURRENT FILING DATE: 2001-08-07
PRIOR APPLICATION NUMBER: 09/183,706
PRIOR FILING DATE: 2001-10-30
NUMBER OF SEQ ID NOS: 43
SEQ ID NO 6
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                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/847,185
FILING DATE: 01-May-2001
CLASSIFICATION: <URKNOWN>
PRIOR APPLICATION DATA:
                                                                                                 ADDRESSEE: CAMPBELL & FLORES, LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.0%; Score 29; DB 10; I
100.0%; Pred. No. 8.9e+04;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815 REFERENCE/DOCKET NUMBER: P-IM 2442 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-847-185-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 09/201,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (619)535-9001
TELEPRAX: (649)535-8949
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/09923831 Patent No. US20020115142A1 GENERAL INFORMATION:
                                                                                                                                                                                                  COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 9 amino acids
                                                    NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
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Matches 5; Conservative
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TITLE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44
FILE REFERENCE: L0461/7104
CURRENT APPLICATION NUMBER: US/09/766,889A
CURRENT FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 60/177,242
PRIOR FILING DATE: 2000-01-20
PRIOR RFILING DATE: 2000-10-25
NUMBER OF SEQ ID NOS: 59
SOFTMARE: FASTESQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Patent No. US/2002012791A1

GENERAL INFORMATION:

APPLICANT: Nicolette, Charles A.

TITLE OF INVENTION: ANTIGENIC CK-18 COMPOUNDS FOR THERAPY

TITLE OF INVENTION: AND DIAGNOSIS AND METHODS FOR USING SAME
FILE REFERENCE: GZ 210800

CURRENT APPLICATION NUMBER: US/10/026,001

CURRENT FILING DATE: 2001-12-21

PRIOR FILING DATE: 2000-12-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 9;
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APPLICANT: Livingston, Brian
APPLICANT: Baker, Denisw
APPLICANT: Newman, Mark
APPLICANT: Newman, David
TITLE OF INVENTION: METODS AND SYSTEM FOR OPTIMIZING
TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY
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Pred. No. 8.9e+04;
1; Mismatches 1;
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Pred. No. 8.9e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 9
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CURRENT APPLICATION NUMBER: US/09/894,018
CURRENT FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: PCT/US00/35568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 319, Application US/09894018
; Patent No. US20020119127A1
                                                                                                                                                                                                                                                                                                                      56.5%;
66.7%;
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Chestnut, Robert
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APPLICANT: EPIMMUNE, INC.
APPLICANT: Sette, Alessan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-026-001-3
                                                                                                                                                                                                                                      TYPE: PRT
CORGANISM: Homo sapiens
US-09-766-889A-7
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
SOFTWARE: Variety (18/09/017,743C
FILING DATE: 03-Feb-1998
CLASSIFICATION VUNBER: US 09/590,298
FILING DATE: 23-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 018623-008050US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 7, Application US/09766889A
; Patent No. US20020164654A1
; GENERAL INFORMATION:
APPLICANT: Luiten, Rosalie
; APPLICANT: Luiten, Rosalie
; APPLICANT: Van der Bruggen, Pierre
; APPLICANT: Stroobant, Vincent
; APPLICANT: Schultz, Erwin
                                                                                          RESULT 12
US-09-017-743C-32
Sequence 32, Application US/09017743C
Patent No. US20020177694A1
GENERAL INFORMATION:
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Best Local Similarity 66.7
Matches 6; Conservative
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ZIP: 94111-3834
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5 IGHLY 9
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Patent No. 5405940
GENERAL INFORMATION:
PAPPLICANT: Boon, Thierry; van der Bruggen, Pierre;
APPLICANT: Boon, Thierry; van der Bruggen, Pierre;
APPLICANT: De Plaen, Etienne; Lurquin Christophe; Traversari, Catia TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM TITLE OF INVENTION: MAGE GENES AND USES THEREOF NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STRRET: 805 Third Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage COMPUTER: IBM PS/2 OPERATING SYSTEM: PC-DOS SOFTWARE: Wordperfect SOFTWARE: Wordperfect APPLICATION DATA: APPLICATION UNBER: US/07/938,334C FILING DATE: 31-AUG-1992
US-09-162-934-3
US-09-061-388-18
US-09-061-66-4847
US-09-165-95-6
US-09-102-928-18
US-09-102-928-18
US-09-461-083-18
US-09-461-083-18
US-09-165-863-3
US-09-165-863-3
US-09-165-863-3
US-08-617-188A-28
US-08-67-188A-28
US-08-67-256-28
US-08-67-256-28
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US-08-67-256-28
US-08-67-256-28
US-09-007-748-28
US-09-007-748-28
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: LUD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Felfe & Lynch STREET: 805 Third Avenue CITY: New York City STATE: New York CLUY IS?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
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Sequence 2, Appli
Sequence 11, Appl
Sequence 17, Appl
Sequence 51, Appl
Sequence 11, Appl
Sequence 3, Appl
Sequence 3, Appl
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18.915 Million cell updates/sec
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Sequence 15,
Sequence 16,
Sequence 16,
Sequence 27,
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2: /cgn2_6/ptcdata/1/laa/5B_COMB.pep:*
3: /cgn2_6/ptcdata/1/laa/6A_COMB.pep:*
4: /cgn2_6/ptcdata/1/laa/6B_COMB.pep:*
5: /cgn2_6/ptcdata/1/laa/pcTUS_COMB.pep:*
6: /cgn2_6/ptcdata/1/laa/pcTUS_COMB.pep:*
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Compugen Ltd.
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US-09-183-931-27
US-09-183-931-33
US-08-393-273E-17
US-09-183-706-6
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US-08-433-341-16
US-08-433-441-15
US-08-334-6702-16
US-08-338-6702-16
US-08-431-1868-16
US-08-687-226-27
US-08-687-226-27
US-08-07-748-27
US-08-07-748-27
US-08-186-266-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            262574 seqs, 29422922 residues
                          GenCore version
Copyright (c) 1993 - 2002
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                  - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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46
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Match
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Perfect score:
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Maximum DB
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TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM
TITLE OF INVENTION: MAGE-3 GENE AND PRESENTED BY HLA-A1 AND USES THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Sequence 15, Application US/08498461
| Sequence 15, Application US/08498461
| Patent No. 5827073
| GENERAL INFORMATION:
| APPLICANT: Luescher, Immanuel; Anjuere, Fabienee;
| APPLICANT: Layer, Andreas; Romero, Pedro; Cerottini, Jean-Charles
| TITLE OF INVENTION: Photoreactive Peptide Derivatives
| NUMBER OF SEQUENCES: 16
| CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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MEDIUM TYPE: Diskette, 3.5 inch, 1.44 kb storage COMPUTER: IBM
                                                                                                                                                                                 COUNTRY: USA
ZIF: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82.6%; Score 38; DB 1; Le
100.0%; Pred. No. 1.9e+05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                              SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,341
FILING DATE: 17-MAY-1995
CLASSIFICATION NUMBER: 08/073,103
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,103
FILING DATE: 7-JUNE-1993
PRIOR APPLICATION NUMBER: 07/938,334
FILING DATE: 31-AUG-1992
PRIOR APPLICATION NUMBER: 08/037,230
APPLICATION NUMBER: 08/037,230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Hanson, No. 5695994man D.
REGISTRATION NUMBER: 30,946
REGISTRATION NUMBER: 1UD 5293.
TELECOMMUNICATION INFORMATION:
TELEPRAN: (212) 688-9200
TELEPRAN: (212) 888-3884
INFORMATION FOR SEQ ID NO: 5EQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/037,230
FILING DATE: 26-MARCH-1993
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
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OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
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                                                                                                                                            New York City
                                                                                                                                                                                                                                                                           COMPUTER: IBM PS/2
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Best Local Similarity
7; Conserve
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TOPOLOGY: lin
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STATE: New 10022
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APPLICANT: De Diaen, Etienne
APPLICANT: De Plaen, Etienne
APPLICANT: De Plaen, Etienne
APPLICANT: De Plaen, Etienne
APPLICANT: Lurquin, Christophe
APPLICANT: Traversari, Catia
APPLICANT: Van den Bynde, Benoit
TITLE OF INVENTION: ISOLATED NONPERPENDES DERIVED FROM
TITLE OF INVENTION: MAGE-3 GENE AND PRESENTED BY HLA-A1 AND USES THEREOF
NUMBER OF SEQUENCES:
ADDRESSE: Felfe & Lynch
STRET: New York City
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: WORDER: C-DUS
SOFTWARE: WORDER: C-DUS
SOFTWARE: WORDER: US/08/073,103A
APPLICATION UNBER: US/08/073,103A
FILING DATE: 7-JUNE-1993
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUBER: 0/938,334
FILING DATE: 31-AGG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Henson, No. 5462871man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5293.1
TELECOMMUNICATION:
MELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boon-Falleur, Thierry
van der Bruggen, Pierre
De Plaen, Etienne
Lurguin, Christophe
Traversari, Catia
                                                                                          Sequence 16, Application US/08073103A Patent No. 5462871 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaugler, Beatrice
Van den Eynde, Benoit
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Patent No. 5695994
GENERALI INFORMATION:
RAPLICANT: BOON-Falleur, Thierry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PC-DOS
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Best Local Similarity 100.،
نابع 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
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STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                            US-08-073-103A-16
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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GENERAL INFORMATION:
APPLICANT: BOON-FALLEUR, Thierry; VAN DER BRUGGEN,
APPLICANT: BLENG, Etienne; LURQUIN, Christophe; TRAVERSARI, Catia;
APPLICANT: GAUGLER, Beatrice; VAN DEN EYNDE, Benoit; ROMERO, Pedro
TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                         Gaps
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                                                                  Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
                                   Pred. No. 1.9e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.6%; Score 38; DB 4; Le
100.0%; Pred. No. 1.9e+05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Fulbright & Jaworski LLP STREET: 666 Fifth Avenue CITY: New York City STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LUD 5293.3
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,273E
FILING DATE: 23-February-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,103
FILING DATE: 7-June-1993
PRIOR APPLICATION NUMBER: 07/938,334
FILING DATE: 31-August-1992
PRIOR APPLICATION NUMBER: 07/937,230
FILING DATE: 31-August-1992
PRIOR APPLICATION NUMBER: 07/037,230
FILING DATE: 26-March-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 622012man D.
REGISTRATION NUMBER: 20,946
REFERENCE/DOCKET NUMBER: LUD 5293
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   Sequence 16, Application US/08393273E Patent No. 6222012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 16, Application US/08443580F; Patent No. 6379901
100.08; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (212) 318-3168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO:
                                                               7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                         1||||||
3 VRIGHLY 9
                                                                                                                              1 VRIGHLY 7
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                                                                                                                                                                                                                                                                                                RESULT 6
US-08-393-273E-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
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Patent No. 6034214
GENERAL INFORMATION:
APPLICANT: Boon, Thierry; van der Bruggen, Pierre;
APPLICANT: Boon, Pierre;
APPLICANT: Boon, Pierre;
APPLICANT: Boon, Pierre;
APPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.6%; Score 38; DB 2; Length 9; 100.0%; Pred. No. 1.9e+05; live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3; Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb storage COMPUTER: IBM PS/2 OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATE:
APPLICATION NUMBER: 07/938,334
FILING DATE: 31-AUGUST-1992
ATTORNEY/AGENT INFORMATION:
NAME: BAER, MADELINE F.
REGISTRATION NUMBER: 36,437
REFERENCE/DOCKET NUMBER: LUD 5293.2
TELEPHONE: (212) 688-9200
STELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-9200
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                                      PAPELICATION NUMBER: US/08/498,461
FILING DATE: 5-JULY-1995
CLASSIFTCATION: 435
GLASSIFTCATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Hanson, No. 5827073man D.
REGISTRATION NUMBER: 30,946
REGISTRATION NUMBER: LUD 5403
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TOPPLOGY: linear
US-08-498-461-15
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/354,679C
FILING DATE: 13-DECEMBER-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.v.,
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STREET: 805 Third Avenue
CITY: New York City
              CURRENT APPLICATION DATA:
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA ZIP: 10022 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
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US-08-354-679C-16
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US-08-354-679C-16
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Sequence 27, Application US/08687226

Patent No. 5686068

GENERAL INFORMATION:
APPLICANT: Melief, Cornelis J. M.; Visseren, M. W.;
APPLICANT: Boon-Falleur, Thierry, Applicant: Boon-Falleur, Thierry applicant: Boon-Falleur, Thierry applicant: Boon-Falleur, Thierry Title OF INVENTION: MagE-2, Cytolytic T Cells Specific To Complexes Of TITLE OF INVENTION: Peptides And HLA-A2 Molecules, And Uses Thereof NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:
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Pred. No. 1.9e+05;
0; Mismatches 1; Indels
                                                                                                               MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage COMPUTER: IBM PS/2 OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/217,188A FILING DATE: 24-MARCH-1994 CLASSIFICATION: 530 ATTORNEY/AGENT INFORMATION: NAME: HARSON, NO. 5554724man D. REGISTATION NUMBER: 30,946 REFERENCE/DOCKET NUMBER: LUD 5340 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Hanson, No. 5686068man D. REGISTRATION NUMBER: 30,946
REFERENCE/DGCKET NUMBER: LUD 5447
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/687,226
FILING DATE: 25-JULY-1996
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08/217,188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 amino acid residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.4%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (212) 688-9200
TELEPAX: (212) 838-384
INFORMATION FOR SEQ ID NO: 27
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
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                                                                                                                                                                                   SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
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                                                                                           COMPUTER READABLE FORM:
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CITY: New York City STATE: New York
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OPERATING SYSTEM: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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                                             USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | |||||
2 ISHLYIL 8
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                                                                 10022
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US-08-687-226-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                             COUNTRY:
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              APPLICANT: Boon-Falleur, Thierry; van der Bruggen, Pierre;
APPLICANT: Boon-Falleur, Etienne; Lurquin Christophe; Traversari, Catia
Gaugler, Beatrice; Van den Eynde, Benoit
TITLE OF INVENTION: Method For Screening For Cancer
Using Binders For MAGE Related Peptides And Complexes
Of The Peptide And HLA Molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
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APPLICANT: Visseren, M. J. W.
APPLICANT: Visseren, M. J. W.
APPLICANT: Van der Bruggen, Pierre
APPLICANT: van der Bruggen, Pierre
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Tumor Rejection Antigen
TITLE OF INVENTION: Precursor MAGE-2 Derived Peptides, and Uses Thereof
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage COMPUTER: IBM, PH.D./2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82.6%; Score 38; DB 4; Length 9; 100.0%; Pred. No. 1.9e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P. STREET: 666 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,580F
FILING DATE: 17-May-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,103
FILING DATE: 31-AUGUST-1993
APPLICATION NUMBER: 07/938,334
FILING DATE: 31-AUGUST-1992
APPLICATION NUMBER: 08/037,230
FILING DATE: 26-MARCH-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Hanson, No. 6379901man D.
REGISTRATION NUMBER: 30,946
REGISTRATION NUMBER: LUD 5293.4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752.5958
INFORMATION FOR SO ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 27, Application US/08217188A Patent No. 5554724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                         CITY: New York City STATE: New York
                                                                                                                                                             NUMBER OF SEQUENCES: 22
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805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 82.6%
Best Local Similarity 100.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                         COUNTRY: USA
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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US-08-217-188A-27
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Gaps

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COUNTRY:
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APPLICANT: Melief, Cornelis J. M.
APPLICANT: Visseren, M. J. W.
APPLICANT: Kast, W. M.
APPLICANT: Van der Bruggen, Pierre
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Tumor Rejection Antigen
TITLE OF INVENTION: Precursor MAGE-2 Derived Peptides, and Uses Thereof
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                     Length 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LUD 5340.1 DIV (081585)
                                                                                                                                                                                   Score 31; DB 1; I
Pred. No. 1.9e+05;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordberfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/667,725B
FILING DATE: 21 June 1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Fulbright & Jaworski LLP
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Hanson, No. 6063900man D.
RECISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5340
TELECOMMUNICATION INFORMATION:
TELEPRAX: (212) 7318-3000
INFORMATION FOR SEQ ID NO: 27: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 27, Application US/08667725B
; Patent No. 6063900
                 INFORMATION FOR SEQ ID NO: 27: SEQUENCE CHARACTERISTICS: LENGTH: 9 amino acid residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 amino acid residues
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                                                                                                                                                                                                                       6; Conservative
                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-687-226-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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Best Local Similarity
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Best Local Similarity
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2 ISHLYIL 8
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|SHLYIL 8
TELEPHONE:
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US-08-667-725B-27
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                                                                                                                                                                                                                      Matches
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RESULT 11

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APPLICANT: Kast; W. M. J. W.
APPLICANT: Kast; W. M. J. W.
APPLICANT: Rast; W. M. J. W.
APPLICANT: Non der Bruggen, Pierre
APPLICANT: Son-Falleur, Thierry
TITLE OF INVENTION: Isolated Tumor Rejection Antigen
TITLE OF INVENTION: Precursor MAGE-2 Derived Peptides, and Uses Thereof
CORRESPONDENCE ADDRESS:
ADDRESSE: Fulbright & Jaworski LLP
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Boon, Thierry; van der Bruggen, Pierre;
APPLICANT: Boon, Thierry; van der Bruggen, Pierre;
APPLICANT: Boon, Thierry; van der Bruggen, Pierre;
APPLICANT: BOON, Eilene, Lurquin Christophe; Traversari, Catia
TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERLYED FROM
TITLE OF INVENTION: MAGE GENES AND USES THEREOF
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STRET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUTER READABLE FORM:
MEDIUTER: Diskette, 5.25 inch, 360 kb storage COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/007,748
FILING DATE: 15 January 1998
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage COMPUTER: IBM PS/2 OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Hanson, No. 6147187man D.
REGISTRATION NOMBER: 30,946
REFERENCE/DOOKET NUMBER: LUD 5340.2 DIV (081572)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 31; DB 4; Le
Pred. No. 1.9e+05;
0; Mismatches 1;
Sequence 27, Application US/09007748
Patent No. 6147187
GENERAL INFORMATION:
APPLICANT: Melief, Cornelis J. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 4, Application US/07938334C
; Patent No. 5405940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.4%;
85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
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New York
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US-07-938-334C-4
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Gaps
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APPLICANT: KUBO, Ralph T.
APPLICANT: GREY, Howard M.
APPLICANT: GELIS, Esteban
TITLE OF INVENTION: INDUCTION OF ANTI-TUMOR CYTOTOXIC
TITLE OF INVENTION: TYMPHOCYTES IN HUMANS USING
TITLE OF INVENTION: SYNTHETIC PEPTIDE EPITOPES
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE:
STREET: Steuart Street Townsend And Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
                                                                                                                                                                                                                               63.0%; Score 29; DB 1; Length 9; 100.0%; Pred. No. 1.9e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Bastian, Kevin L.
RECISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 14137-50-4
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDUUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08186266 Patent No. 5662907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 5; Conservative
     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-186-266-2
                                                           TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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5 IGHLY 9
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CITY: Sa
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US-08-186-266-2
                             LENGTH:
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Patent No. 5462871
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: boon-Falleur, Thierry
APPLICANT: borland, Eleane
APPLICANT: Lurquin, Christophe
APPLICANT: Traversari, Catia
APPLICANT: Traversari, Catia
APPLICANT: Gauglar, Bearince
APPLICANT: Van den Eydde, Benoit
TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM
TITLE OF INVENTION: MAGE-3 GENE AND PRESENTED BY HLA-A1 AND USES THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.0%; Score 29; DB 1; Length 9; 100.0%; Pred. No. 1.9e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLION TITE: DISKETCE, 5.25 INCH, 360 COMPUTER: IBM PS/2 OPERATING SYSTEM: PC-DOS OPERATING SYSTEM: PC-DOS SOCTWARE: Wordperfect CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/073,103A FILING DATE: 7-JUNE-1993 CLASSIFCATION: 435 PRIOR APPLICATION A35 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/938,334 FILING DATE: 31-AUG-1992 ATTORNEY, AGENT INFORMATION: NAME: HARSON, NO. 5462871man D. REGISTRATION NUMBER: 30,946 REFERENCE/DOCKET NUMBER: 10D 5293.1 TELECOMMUNICATION: TELECOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: MAGE-3 derived nonapeptide
                                            FILING DATE: 31-AUG-1992
CLASSFFICATION: 435
                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: Hanson, No. 5405940man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 293
TELECOMMUNICATION INFORMATION:
TELEPAX: (212) 889-9200
TELEPAX: (212) 88-384
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acid residues
TYPE: amino acid residues
TYPE: amino acid residues
TYPE: amino acid residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ...LAKESEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (212) 688-9200
TFLEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 10v.,
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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| S IGHLY 9
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Search completed: December 19, 2002, 16:46:00 Job time : 15 secs

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                                                                                                                                                                                                                                                                                                                        APPLICANT: RUBO, Ralph T.
APPLICANT: GREY, Howard M.
APPLICANT: SETTE, Alessandro
APPLICANT: SETTE, Alessandro
APPLICANT: SETTE, Alessandro
TITLE OF INVENTION: INDUCTION OF ANTI-TUMOR CYTOTOXIC
TITLE OF INVENTION: TIMPHOCYTES IN HUMANS USING
TITLE OF INVENTION: SYMHETIC PEPTIDE EPITOPES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
CITY: California
  63.0%; Score 29; DB 1; Length 9; 100.0%; Pred. No. 1.9e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
63.0%; Score 29; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CUUNTRY: CALILORNIA

CUNTRY: CALILORNIA

21P: 94105-1493

COMPUTER READRABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPAtible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/186,266

CLASSITCATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/159,339

FILING DATE: 25-NOV 1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/027,746

FILING DATE: US-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: BASILAN, KEVIN L.

REGISTRATION NUMBER: 34,774

REFERENCE/DOCKET NUMBER: 14137-50-4

TELECOMMUNICATION INFORMATION:

NAME: BASILAN, KEVIN L.

REFERENCE/DOCKET NUMBER: 14137-50-4
                                                                                                                                                                                                                                                          Sequence 11, Application US/08186266; Patent No. 5662907
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 9 amino acids
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Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                           3 IGHLY 7
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5 IGHLY 9
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TOPOLOGY:
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December 19, 2002, 16:45:43 ; Search time 34 Seconds (without alignments) 39.191 Million cell updates/sec
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                      908470 segs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maximum Match 100%
Listing first 45 summaries
                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
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Result		Query	Query			
Q	Score	Match	Length	DB	ID	Description
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4	2	TOO. C	7	77	AAEU2083	MAGE-Al2 human leu
7	46	92.0	σ	22	AAE12995	Himan MAGE-12 T-CP
m	46	92.0	6	22	AAE02082	MAGE-A12 himan len
4	42	84.0	œ	22	AAE02084	MAGE-A12 human 1cu
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7	42	84.0	σ	20	AAY46062	Imminogenic nentid
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RESULT 1

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Human; cytostatic; immunogen; MAGE-Al2; human leukocyte antigen; HLA;
CD8; cytotoxic T lymphocyte; cancer; carcinoma; melanoma; myeloma;
brain tumour; sarcoma; vaccine; gene therapy.
                                                                                                                                                                                                                                                                     Brasseur
                                                                  MAGE-A12 human leukocyte antigen-binding peptide #3.
                                                                                                                                                                                                                                                                   Boon-Falleur T,
        AAE02083 standard; peptide; 10 AA.
                                                                                                                                                                                                                                              (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                   Van Den Eynde B,
                                                                                                                                                                                                               19-OCT-1999; 99US-0160374.
01-FEB-2000; 2000US-0179570.
                                                                                                                                                                                            19-OCT-2000; 2000WO-US28852.
                                                 (first entry)
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                                                                                                                                                   WO200129220-A2.
                                                                                                                                  Homo sapiens,
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                                                31-JUL-2001
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                             AAE02083;
AAE02083
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New antigenic peptides derived from MAGE-A12 polypeptides, useful for diagnosis and treatment of cancer, such as bladder, lung, breast,

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RESULT
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                                                          protein and presented by human leukocyte antigens (HLAA). These antigenic peptides when presented by an antigen presenting cell having a HLAA class I molecule, effectively induce the activation and proliferation of CD8+ cytocker T lymphocytes. MAGE-A12 is useful for treating a subject having a disorder characterised by expression of MAGE-A12. The protein microarray comprising MAGE-A12 is useful for diagnosing a disorder, especially cancer, by determining the binding of an antibody, T lymphocytes or a HLA molecule isolated from the subject suspected of having the disorder characterised by the expression of MAGE-A12 is useful for treating cancers, including bladder carcinomas, melanomas, oesophageal, lung, head and cneck, breast, colorectal carcinomas, myelomas, brain tumours, sarcomas, prostate and renal carcinomas and to produce antibodies. MAGE-A12 antibodies are useful for diagnosing disorders characterised by expression of MAGE-A12 immunogenic polypeptide. These MAGE-A12 carcinomas and to produce antibodies. MAGE-A12 carcinomas and so used in gene therapy.

The present sequence is MAGE-A12 HLA class I-binding peptide. This antipodie is presented by major histocompatibility complex.
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                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated and purified T cell epitope of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel T cell epitope of MAGE-12 is a tumor rejection antigen for melanoma expressing HLA-Cw0702 recognized by tumor-infiltrating lymphocytes and useful to treat cancer particularly melanoma
                                                                                                                                                                                                                                                                                                                                                                                             .,
                                                     patent discloses antigenic peptides derived from MAGE-Al2
                                                                                                                                                                                                                                                                                                                                                               Length 10;
                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 50; DB 22;
100.0%; Pred. No. 0.00086;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marincola F;
brain, prostate and renal carcinomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE12995 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                             is recognised by CTLs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Člaim 1; Page 14; 17pp; English.
                            claim 2; Page 42; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human MAGE-12 T-cell epitope.
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Best Local Similarity 100.0
Watches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                    10 AA;
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                                                                                                                                                                                                                                                                                                             (MHC) and
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AAE12995
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The patent discloses antigenic peptides derived from MAGE-A12
protein and presented by human leukocyte antigens (HLAS). These
antigenic peptides when presented by an antigen presenting cell
antigenic peptides when presented by an antigen presenting cell
having a HLA class I molecule, effectively induce the activation
condition of CD8+ cytotoxic T lymphocytes. MAGE-A12 is
useful for treating a subject having a disorder characterised by
expression of MAGE-A12. The protein microarray comprising MAGE-A12
is useful for diagnosing a disorder, especially cancer, by determining
the binding of an antibody. T lymphocytes or a HLA molecule isolated
from the subject suspected of having the disorder characterised by the
corporation of MAGE-A12. MAGE-A12 is useful for treating cancers,
including bladder carcinomas, melanomas, oseophageal, lung, head and
neck, breast, colorectal carcinomas, myelomas, brain tumours, sarcomas,
prostate and renal carcinomas and to produce antibodies. MAGE-A12
antibodies are useful for diagnosing disorders characterised by
carcinesion of MAGE-A12 immunogenic polypeptide. These MAGE-A12
expression of MAGE-A12 immunogenic polypeptide. These MAGE-A12
expression of waccines. They are also used in gene therapy.
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MAGE-12. MAGE-12 is a tumour rejection antigen for melanoma which expresses MHC-class I molecule HLA-Cw0702 recognised by tumourinfiltrating lymphocytes. The epitope or a vector encoding the epitope is used to treat cancer, particularly melanoma expressing HLA-Cw asterisk 0702. The epitope has widespread utility in cancer immunotherapy since MAGE-12 is mostly found in tumours. The present sequence is human MAGE-12 T-cell epitope.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antigen; HLA;
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100.0%; Pred. No. 7.8e+05;
ive 0; Mismatches 0;
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Gaps

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Score 42; DB 22; I Pred. No. 7.8e+05; 0; Mismatches 0;

84.0%; Scor. 100.0%; Pre

8; Conservative

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Similarity

8 AA;

Length 8; Indels

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Sequence
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The present sequence is MAGE-A12 HLA class-I-binding peptide. This antigenic peptide is presented by major histocompatibility complex. (MHC) and is recognised by CTLS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; cytostatic; immunogen; MAGE-A12; human leukocyte antigen; HLA;
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The present sequence is MACE-Al2 HLA class-I-binding peptide. This antigenic peptide is presented by major histocompatibility complex (MHC) and is recognised by CTLs.
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                                                                                                                                                   92.0%; Score 46; DB 22; Length 9; 100.0%; Pred. No. 7.8e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAGE-A12 human leukocyte antigen-binding peptide #4.
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                                                                                                                                                                                                                                                                                                                                                                                                                           AAE02084 standard; peptide; 8 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (LUDW-) LUDWIG INST CANCER RES
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01-FEB-2000; 2000US-0179570.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        An isolated nonapeptide having the amino acid sequence Glu-Val-Asp-Pro-Ile-Gly-His-Leu-Tyr is derived from the tumour rejection antigen precursor encoded by the MAGE-3 gene and presented by HLA-A1. The nonapeptide can be used in a vaccine to treat a cancerous condition involving HLA-A1 subtype cancerous cells. The nonapeptide can be used as a probe to identify tumour cells. This sequence is homologous to the peptide described and is encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nona:peptide derived from tumour rejection antigen precursor - presented by HLA-Al cancer cells, for use in diagnosis or therapy of esp. melanoma and breast cancer.
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0
                                                                                                                                                                                                                                                MAGE; nonapeptide; cancer; melanoma; breast cancer; HLA;
histocompatability; human leucocyte antigen; probe; treatment;
therapy; vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           De Plaen E, Lurquin C, Traversari C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 20; 33pp; English.
                                            AAR50283 standard; Protein; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LUDW-) LUDWIG INST CANCER RES
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93US-0037230.
93US-0073103.
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                                                                                                                                              (first entry)
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Matches 8; Conservative
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N-PSDB; AAQ44753.
                                                                                                                                                                                                MAGE-21 nonapeptide
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Van Derbruggen P;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-AUG-1993;
                                                                                                                                              26-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-AUG-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                   WO9405304-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAR-1993
                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                            AAR50283;
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RESULT 5
                       AAR50283
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2 VVRIGHLY
                                                                                                                                                     Homo sapiens.
             01-DEC-1999
                                                                                                                                                                            W09945954-A1
                                                                                                                                                                                                                              13-MAR-1998;
                                                                                                                                                                                                                                                     13-MAR-1998;
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                                                                                                                                                                                                     16-SEP-1999.
                                                                                                                                        Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rejection antigen region of the full length MAGE sequences. These peptides were used to design the nonapeptides of the invention (see AAR9937-R9942), which bind to a HLA molecule on a cell, and provoke 1ysis by cytolytic T cells (CTLS) specific for a complex of the HLA molecule and nonapeptide. The nonapeptides can be used diagnostically to identify tumours expressing a particular HLA molecule, or to identify cancer cells. The peptides can also be used therapeutically, to induce a tesponse to tumours (where the peptides are optionally coupled to tumour-specific antibodies), or to induce a response by CTLs that are otherwise inactive. The peptide sequences may also be used to expand specific CTLs in vitro for later return to the patient, such as for treating melanoma. Tumour cells can be identified by using DNA encoding the nonapeptides as probes. Non-human cells transformed with the HLA Algene and a DNA sequence encoding one of the peptides, can be used to generate CTLs, or to detect the presence of CTLs in human samples. The non-human transformed cells, when polytransformed, are universal effector cells, and can be used in vaccines, or for treating melanoma or breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                              HIA binding peptide; cell lysis; cytolytic T cell; MAGE tamily; numan; tumour rejection antigen precursor; TRA; MAGE-1; tumour; cancer cell; antibody; melanoma; universal effector cell; vaccine; breast cancer; CTL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                         New nona:peptide(s) that bind to HLA molecule(s) and induce lysis by specific cytolytic T cells, for diagnosis and treatment of tumours and to expand T cells in vitro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR99343-R99350 represent MAGE nonapeptides, based on the tumour
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                                                                                                                                                                                                                                                                                                                  Lurquin C;
Van Der Bruggen P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84.0%; Score 42; DB 17; Length 9; 100.0%; Pred. No. 7.8e+05; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                  Boon-Falleur T, De Plaen E, Gaugler B, I
Romero P, Traversari C, Van Den Eynde B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY46062 standard; Peptide; 9 AA.
AAR99345 standard; Protein; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 4; Fig 4; 41pp; English.
                                                                                                                                                                                                                                                                                         (LUDW-) LUDWIG INST CANCER RES.
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                                                                                                                                                                                                                                        96WO-US01489
                                               22-APR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-402317/40.
                                                                        MAGE-21 nonapeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAT35410.
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                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                        01-FEB-1996;
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                                                                                                                                                                                       WO9626214-A1
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                                                                                                                                        therapy
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AAY45390 to AAY48214 represent specifically claimed immunogenic peptides having a human major histocompatibility complex (MHC) Class I (also known as human leukocyte antigen (HLA) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes CE HLA-A2.1, Al. A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived.

Cytotoxic T lymphocytes (CTLS) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound or an HLA molecule, rather than the intact foreign antigen itself, and are particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) cray prevent viral infections and cancers in mammals (especially humans) they can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or individuals susceptible or otherwise at risk of viral infection or useful diagnostically, and can be used to induce a cytotoxic T cell response, by contacting a cytotoxic T cell with the peptide e.g. to produce CTLs av vivo for infusion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful thempeutically and for immunisation as above.
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                                                                                   Immunogenic peptide having a human leukocyte antigen binding motif #673
                                                                                                                                                             Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
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100.0%; Pred. No. 7.8e+05;
ive 0; Mismatches 0;
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(first entry)
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                   vaccine; immunisation.
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transfectants.
                                                Homo sapiens
                                                                                                                                 05-FEB-1997;
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                                                                                                     28-AUG-1997.
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AAY47343
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                                                                                                                                                                                                                                                                                                                                                                                                                       The patent discloses antigenic peptides derived from MAGE-A12 protein and presented by human leukocyte antigens (HLAs). These antigenic peptides when presented by an antigen presenting cell having a HLA class I molecule, effectively induce the activation and proliferation of CD8+ cytocoxic I lymphocytes. MAGE-A12 is useful for treating a subject having a disorder characterised by expression of MAGE-A12. The protein microarray comprising MAGE-A12 is useful for diagnosing a disorder, especially cancer, by determining the binding of an antibody. I lymphocytes or a HLA molecule isolated from the subject suspected of having the disorder characterised by the expression of MAGE-A12. MAGE-A12 is useful for treating cancers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               including bladder carcinomas, melanomas, oceophageal, lung, head and neck, breast, colorectal carcinomas, myelomas, brain tumours, sarcomas, prostete and renal carcinomas and to produce antibodies. MAGE-Al2 antibodies are useful for diagnosing disorders characterised by expression of MAGE-Al2 immunogenic polypeptide. These MAGE-12 peptides are useful sequence is MAGE-Al2 immunogenic polypeptide. These MAGE-12 peptides are useful sequence is MAGE-Al2 immunogenic polypeptide. These MAGE-12 peptides are useful sequence is MAGE-Al2 immunogenic polypeptide. These MAGE-I2 peptides are useful sequence is MAGE-Al2 HLA class I-binding peptide. This antigenic peptide is presented by major histocompatibility complex (MHC) and is recognised by CTLS.
                                       Human; cytostatic; immunogen; MAGE-A12; human leukocyte antigen; HLA;
CD8; cytotoxic T lymphocyte; cancer; carcinoma; melanoma; myeloma;
brain tumour; sarcoma; vaccine; gene therapy.
                                                                                                                                                                                                                                                                                                                                      New antigenic peptides derived from MAGE-A12 polypeptides, useful for diagnosis and treatment of cancer, such as bladder, lung, breast,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 7.8e+05;
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          MAGE-A12 human leukocyte antigen-binding peptide #1.
                                                                                                                                                                                                                                                                                     Boon-Falleur T,
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                     brain, prostate and renal carcinomas
                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 42; 69pp; English.
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100.08; Pic
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                                                                                                                                                                                                                                                      (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                        01-FEB-2000; 2000US-0179570.
                                                                                                                                                                               .9-OCT-2000; 2000WO-US28852
                                                                                                                                                                                                                99US-0160374
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Quest Local Similarity 100.vv
Best Local 8; Conservative
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                                                                                                                         WO200129220-A2.
                                                                                               Homo sapiens
                                                                                                                                                                                                           19-0CT-1999;
                                                                                                                                                       26-APR-2001.
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Immunogenic peptide having a human leukocyte antigen binding motif #1954.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human leukocyte antigen B44 positive cells for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
human leukocyte antigen B44; cytotoxic T lymphocyte; cancer; melanoma; therapy; diagnosis; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84.0%; Score 42; DB 18; Length 10; 100.0%; Pred. No. 0.038; 1ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                               Herman J, Luescher I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumour rejection antigens presented by molecules - useful to identify HLA-B44 and therapy of cellular abnormalities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY47343 standard; Peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.0°,
100.0%; Pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 51; 74pp; English.
                                                                                                                                                                                                                                                                                                                                         (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                        96US-0602506.
                                                                                                                                                                                                                                    97WO-US01915.
                                                                                                                                                                                                                                                                                                                                                                                               Coulie P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-435086/40.
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                        Van Der Bruggen P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 VVRIGHLY 10
                                                                                                                                                                                                                                                                                                                                                                                             Boon-Falleur T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VVRIGHLY 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9945954-A1
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28-JUN-2000; 2000WO-US17842.
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                                                                                                         Fikes J,
Keogh E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB76152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB76152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      οy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anion a human major histocompatibility complex (MHC) class I class I charlon a human major histocompatibility complex (MHC) class I class I charlon a specific HLA binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-AZ.1, Al, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived.

Cytotoxic T lymphocytes (CTLS) which destroy antigen bearing cells are normally induced by an antigen from of a peptide fragment bound to maily induced by an antigen in the form of a peptide fragment bound to remaily induced by an antigen in the form of a peptide fragment bound to are particularly important in the motor celection and in fighting viral infections and cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B and C, ALDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                          to AAY48214 represent specifically claimed immunogenic peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; human leukocyte antigen; HLA epitope; cytotoxic T lymphocyte;
CTL; MAGE2; MAGE3; melanoma antigen gene; immune response; vaccine;
cancer; cytostatic; immunostimulant.
                                                                                                                                                                                                                                                                                       New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases {}^{-}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 response, by contacting a cytotoxic T cell with the peptide e.g. to produce CTLs ex vivo for infusion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                  Southwood S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37; DB 20; Length 10; Pred. No. 0.41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                     Grey HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapeutically and for immunisation as above.
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                                                                                                                                                                                                     Celis E,
                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 104; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG84743 standard; Peptide; 9 AA.
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                                                                                                                                                                                                       Sette A, Kubo RT, Sidney J,
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80.0%;
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                                                             98WO-US05039.
                                                                                                           98WO-US05039
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                                                                                                                                                        (EPIM-) EPIMMUNE INC
                                                                                                                                                                                                                                               WPI; 1999-551214/46.
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                                                             13-MAR-1998;
                                                                                                           13-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JUN-2001.
                     16-SEP-1999,
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                                                                                                                                                                                                                                                                                                                                                                                                          AAY45390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG84743
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The present invention describes MAGE2/3 epitopes (I). Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is cultured in vivo and binds to a complex of (I); (2) a peptide (II) comprising (I) and a second epitope and has less than 50 contiguous amino acids; (3) a vaccine composition comprising (II), a unit dose of a peptide with at least 50 contiguous amino acids with 100% identify to the native peptide sequence of MAGE2/3, and a pharmaceutical excipient; (4) an isolated nucleic acid encoding (II); and (5) an isolated nucleic acid encoding (II). (I) has encoding (I); and (5) an isolated nucleic acid encoding (II). (I) has cytostatic activity, and can be used in vaccines and as an immunostimulant. A vaccine of (3) is useful for the treatment and prevention of cancer. (I) is useful for monitoring or evaluating an immune response by incubating a T-lymphocyte ample from a patient with compined and detecting the presence of the T-lymphocyte that binds to the patient and detecting the presence of the T-lymphocyte that binds to the peptide. The vaccine allows the opportunity to combine epitopes derived trom multiple tumour-associated molecules reducing the likelihood of tumour escape due to antigen loss. AAG84515 to AAG84909 and AAB99725 concept in month, and the present and the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                          An isolated prepared MAGE2/3 epitope (I) for use in pharmaceuticals for the treatment and prevention of cancer -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                 Celis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 35; DB 22; Length 9; Pred. No. 7.8e+05; 1; Mismatches 0; Indels
                                                                                                                                                                 Southwood S, Chesnut R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumour associated antigen MAGE3 immunogenic peptide.
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                                                                                                                                                                      Sette A, Sidney J,
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85.7%;
99US-0458298
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Matches 6; Conservative
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                                                                              (EPIM-) EPIMMUNE INC.
                                                                                                                                                                                                                                                                                                WPI; 2001-375002/39.
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New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases \cdot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY46232;
                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a composition (I) which comprises at least one human leukocyte antigen (HLA) binding peptide comprising an isolated, prepared epitope comprising one of 547 %-11 residue amino acid sequences (SI), given in AAB75803 to AAB76349. (I) has cytostatic, virucide, hepatotropic, antiinflammatory, anti-HIV (human immodeficiency virus) and protozoacide activities, which can be used in vaccine production and is an inducer of cytotoxic T-cell response. (I) is useful for inducing a cytotoxic T cell response against a present antigen in a patient expressing a specific major istocompatibility complex (MHC) class I allele, by contacting cytotoxic T cells (CTLS) from the patient with (I). (I) is useful as a vaccine to treat and/or prevent viral infection and cancer such as prostate cancer, bepatitis B, hepatitis C, human papilloma virus (HPV) infection, cytomegalovirus (CMV), acquired immunodeficiency syndrome (AIDS), renal carcinoma, carvical carcinoma, lymphoma, malaria, and condyloma
                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HLA molecule; cytotoxic T cell; immunogenic peptide; binding affinity;
                                                                                             Composition comprising human leukocyte antigen binding peptide which comprises isolated, prepared epitope useful for treating viral infections such as acquired immunodeficiency syndrome, and cancer -
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAGE-2 170 peptide with binding affinity for HLA-B7-like molecules.
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                                                                                                                                                                                                                                                                                                                                                                         70.0%; Score 35; DB 22; Length 9; 85.7%; Pred. No. 7.8e+05; 1ve 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW45704 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sidney J;
                                                                                                                                         Claim 1; Page 48; 58pp; English.
          99US-0141422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96US-0013113,
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                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 85.7 les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sette A,
                               (EPIM-) EPIMMUNE INC.
                                                   Sette A, Sidney J,
                                                                         WPI; 2001-112389/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-470637/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CYTE-) CYTEL CORP.
                                                                                                                                                                                                                                                                                                                                                    9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                    4 IGHLYIL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                  3 IGHLYII 9
          29-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-JUN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9733602-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-MAR-1996;
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                                                                                                                                                                                                                                                                                                                                 acuminatum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW45704
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This sequence represents an immunogenic peptide with binding affinity for HLA-B7-like molecules. A cytotoxic T cell (CTL) response against a partient by contacting a CTL with pertiate of 9-15 amino acids which binds to at least two an immunogenic peptide of 9-15 amino acids which binds to at least two conductors a cytotoxic T cell response. The immunogenic peptide has a sequence of 9 amino acids, comprising a binding motif, with from the N-to C-termini: primary anchor sites (PAR) at positions 2 (selected from Ala, Leu, Ile, Val, Met, Ser or Thr) and 9 (Arg or Lys) and at least one secondary anchor sites (SAR), i.e. Tyr, Phe or Trp at positions 3, 6 or 5, and/or pro at position 8. The immunogenic peptides are used in peptide based vaccines and therapeutic compositions, for treating viral, pared to fungal diseases or cancer, e.g. prostatic cancer, hepatidis or condyloma acuminatum. They can also be used to elicit a CTL response or vivial cancer return of the cells to the patient, e.g. where the patient does not respond to peptide vaccines or other therapies.

Check the patient does not respond to peptide vaccines or other therapies.

Selection of specific residues for PAR and SAR results in higher binding contactine acuminatum in the patient of pared immunogenicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunogenic peptide having a human leukocyte antigen binding motif #843.
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Inducing cytotoxic T cell response against specific antigen - using immunogenic peptide with binding affinity for HLA-A3-like molecules, to treat or prevent tumours and infections by virus, parasites etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 33; DB 18; Length 9;
Pred. No. 7.8e+05;
0; Mismatches 2; Indels
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                                                                                                                                                                    English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sette A, Kubo RT, Sidney J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66.0%;
77.8%;
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                                                                                                                                                       Example 2; Page 51; 79pp;
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Best Local Similarity
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                                                                                                                                                    AAY45390 to AAY48214 represent specifically claimed immunogenic peptides having a human major histocompatibility complex (MHC) Class I (also knowing a human leukocyte antigen (HLA) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLAA subtypes HLAA21, Al, A3.2 or A24.1 or HLAAB or C) and induce a cytotoxic T cesponse against the antigen from which the peptide is derived.

The consideration of the consideration of a peptide fragment bound or mormally induced by an antigen in the form of a peptide fragment bound are particularly important in the form of a peptide fragment bound are particularly important in the mount rejection and in fighting viral infections and cancers in mammals (especially humans) or prevent viral infections and cancers in mammals (especially humans).

They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell response, by contacting a cytotoxic T cell with the peptide e.g. to produce CTLS ex vivo for infusion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                   Claim 1; Page 62; 150pp; English.
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having a human major histocompatibility complex (WHC) Class I (also known as human leukocyte antigen (HLA) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes C peptides can bind to a specific HLA allele (i.e. HLA-A subtypes CHA-A2.1, A1, A3.2 or A2-L1 or HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived.

Cytotoxic T lymphocytes (CTLS) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen itself, and a perticularly induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen itself, and a perticularly induced by an entigen in mammals (especially humans) cor prevent viral infections and cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B and C, AIDS, and rand mendication or individuals susceptible or otherwise at risk of viral infection or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell with the peptide e.g. to produce CTLs ex vivo for infusion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
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100.0%; Pred. No. 7.8e+05;
ive 0; Mismatches 0;
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Best Local Similarity 100.u
نامع 6; Conservative
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3 IGHLYI 8
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us-09-692-401-5.closed.rapb

Run on:

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Best_Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
IGHLYI 8
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                                                                                                                                                                                                                                                                                                       US-09-766-889A-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-766-889A-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 58
LENGTH: 9
TYPE: PRT
Query Match
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 58, Appl Sequence 67, Appl Sequence 67, Appl Sequence 115, Appl Sequence 116, Appl Sequence 100, Appl Sequence 56, Appl Sequence 23, Appl Sequence 20, Appl Sequence 6, Appl Sequence 7, Appl Sequence 3, Appl Sequence 3, Appl Sequence 32, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 6, Appli
                                                         December 19, 2002, 16:51:44; Search time 10 Seconds (without alignments) 16.764 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
    GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-09-017-743C-30
US-09-017-743C-67
US-09-017-743C-115
US-09-017-743C-31
US-09-017-743C-31
US-09-017-743C-31
US-09-017-743C-31
US-09-017-743C-31
US-09-766-889A-56
US-09-923-831-6
US-09-923-831-6
US-09-923-831-8
US-09-923-831-8
US-09-017-743C-32
US-09-017-743C-32
US-09-017-743C-32
US-09-017-743C-32
US-09-017-743C-32
US-09-016-889A-7
                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                  106657 seqs, 16763532 residues
                                                                                                                                                                                                                                                                          Published_Applications_AA:*
                                                                                                                                                                                                                                  Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                        OM protein - protein search, using sw model
                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
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50
1 VVRIGHLYIL 10
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0 Maximum DB seq length: 10
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                                                                                                                                      Scoring table:
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Result Ņ

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APPLICANT: Luiten, Rosalie
APPLICANT: Luiten, Rosalie
APPLICANT: Luiten, Rosalie
APPLICANT: Boon-Falleur, Thierry
APPLICANT: Stroobant, Vincent
APPLICANT: Stroobant, Vincent
APPLICANT: Schulz, Erwin
TITLE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B44
FILE REFERENCE: Lo461/7104
CURRENT APPLICATION NUMBER: US/09/766,889A
CURRENT APPLICATION NUMBER: US 60/177,242
PRIOR FILING DATE: 2000-01-20
PRIOR FILING DATE: 2000-01-20
PRIOR FILING DATE: 2000-10-25
NUMBER OF SEQ ID NOS: 59
SOFTWARE FASSEQ for Windows Version 3.0
                            Sequence 24, Appl.
Sequence 38, Appl.
Sequence 13, Appl.
Sequence 13, Appl.
Sequence 538, App.
Sequence 708, App.
Sequence 708, App.
Sequence 138, App.
Sequence 346, App.
Sequence 521, App.
Sequence 521, Appl.
Sequence 1, Appl.
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                        US-09-826-290-24
US-09-826-290-24
US-09-816-290-95
US-09-017-43C-38
US-09-791-378-538
US-09-791-378-538
US-09-779-308-708
US-09-779-308-439
US-09-779-308-439
US-09-779-308-439
US-09-779-308-439
US-09-779-308-439
US-09-779-308-439
US-09-779-308-521
US-09-779-308-521
US-09-779-308-521
US-09-779-308-521
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US-09-756-875-16
US-09-756-875-17
US-09-756-983-6
US-09-756-983-13
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US-09-996-288-98
US-09-996-288-110
US-09-996-288-117
                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 58, Application US/09766889A Patent No. US20020164654A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 30, Application US/09017743C
Patent No. US20020177694A1
GENERAL IMFORMATION:
APPLICANT: Sette, Alessandro
Conservative
                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-017-743C-30
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Score 33; DB 9; Length 9;
Pred. No. 8.9e+04;
0; Mismatches 2; Indels
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Sidney, John
Southwood, Scott
TITLE OF INVENTION: HLA Binding Peptides and Their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRASESO for Windows Version 2.0
CURRENT APPLICATION DATA:
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 018623-008050US
                                                                                                                                                                                                        NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 018623-008050US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/017,743C
FILING DATE: 03-Feb-1998
CLASSIFICATION: <Unknown>
                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/017,743C
FILING DATE: 03-Feb-1998
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/590,298
FILING DATE: 23.4AN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/590,298
FILING DATE: 23-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
;
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-017-743C-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-017-743C-115
; Sequence 115, Application US/09017743C
; Patent No. US/0020177694A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
                                                                                                                                                                                                                                                                                                                    TELEFAX: 415-576-0300
TELER: 405-576-0300
TELEX: 405-576-0300
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 66.0
Best Local Similarity 77.8
Matches 7; Conservative
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ZIP: 94111-3834
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77.8%; Pred. No. 8.9e+04;
2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 146
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Sette, Alessandro
Sidney, John
Southwood, Scott
TITLE OF INVENTION: HLA Binding Peptides and Their
                          Southwood, Scott
TITLE OF INVENTION: HLA Binding Peptides and Their
Uses
                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OMPUTER: IBM compatible
OMPUTER: IBM compatible
OMPUTER: IBM compatible
OMPUTER: IBM compatible
SOFTWARE: FastSEQ for Windows Version 2.0
CURRIT APPLICATION DATA:
APPLICATION NUMBER: US/09/017,743C
FILING DATE: 03-Feb-1998
FILING DATE: 23-JAN-1996
ATTORNEY AGENT INFORMATION:
NAME: PATENT INFORMATION:
REGISTRATION NUMBER: 42,058
REGISTRATION NUMBER: 42,058
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 67, Application US/09017743C Patent No. US20020177694A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 415-576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 30:
                                                                                               NUMBER OF SEQUENCES: 146
                                                                                                                                                                                        CITY: San Francisco
    Sidney, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Conservative
                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                             STATE: CA
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APPLICANT: Boon-Falleur, Thierry
APPLICANT: van der Bruggen, Pierre
APPLICANT: van der Bruggen, Pierre
APPLICANT: Demotte, Nathalie
APPLICANT: Demotte, Nathalie
TITLE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44
FILE REFERENCE: L0461/7104
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                                                                                                                                                                     APPLICANT: Sette, Alessandro
Sidney, John
Southwood, Scott
TITLE OF INVENTION: HLA Binding Peptides and Their
                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: USA

COMPUTER: USA

COMPUTER: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: TOWN COMPUTER: OSS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/017,743C
FILING DATE: 03-Feb-1998
CLASSIFICATION ON CURROWN>
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 23-JAN.1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 018623-008050US
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 100: US-09-017-743C-100
                                                                                                         Sequence 100, Application US/09017743C Patent No. US20020177694A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18, Application US/09766889A, Patent No. US20020164654A1, GENERAL INFORMATION:
APPLICANT: Luiten, Rosalie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: <Unknown>
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        3 ISHLYIL 9
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Matches
                                                                      RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Sette, Alessandro
Sidney, John
Southwood, Scott
TITLE OF INVENTION: HLA Binding Peptides and Their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/017,743C
FILING DATE: 03. Feb-1998
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 018623-008050US
                                                                                                                                                                                                           6
                                                                                                                                                                                                         Score 33; DB 9
Pred. No. 0.79;
                                                                                                                                                                                                                                                  Mismatches
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APPLICATION NUMBER: US 08/590,298
FILING DATE: 23-JAN-1996
ATTORNEY/AGBNT INFORMATION:
                                                                                                                        MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 115:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-017-743C-31
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 31, Application US/09017743C Patent No. US20020177694A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and
                                    LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
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ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
INFORMATION FOR SEQ ID NO: 115:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 31: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                         66.0%;
77.8%;
                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 146
                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                 Query Match
Best Local Similarity 77.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 62.0
Best Local Similarity 85.7
Matches 6; Conservative
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US-09-017-743C-31
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APPLICANT: SOO HOO, William
TITLE OF INVENTION: MEMBARARE-BOUND CYTOKINE COMPOSITIONS
COMPRESING GM-CSF AND METHODS OF MODULATING AN IMMUNE
RESPONSE USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT BACKOCKIN, William
APPLICANT BACKOCKIN, William
APPLICANT Wallner, Barbara
TITLE OF INVENTION: STIMULATION OF HEMATOPOIETIC CELLS IN
TITLE OF INVENTION: VITRO
FILE REFERENCE: 10248/7015
CURRENT APPLICATION NUMBER: US/09/812,528
CURRENT PILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: US 60/060,306
PRIOR APPLICATION NUMBER: US 92/162,934
PRIOR FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FASISEO for Windows Version 3.0
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                                                                                                                                                                                                  Length 9;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL & FLORES, LLP
STREET: 4770 La Jolla Village Drive, Suite 700
CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.0%; Score 29; DB 10; I
100.0%; Pred. No. 8.9e+04;
Live 0; Mismatches 0;
    PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27
                                                                                                                                                                                                Score 29; DB 9; L
Pred. No. 8.9e+04;
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100.0%; Pred. No. w...
'... 0; Mismatches
                        NUMBER OF SEQ 1D NOS: 114
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ 1D NO 51
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 23, Application US/09847185 Patent No. US20020076392A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              US-09-812-528-3
; Sequence 3, Application US/09812528
; Patent No. US20010018210A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: California
COUNTRY: United States
ZIP: 92121
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 58.0
Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                            Query Match
Best Local Similarity
5; Conserva
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5 IGHLY 9
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                                                                                                                                                      US-09-909-460-51
                                                                                                                                                                                                                                                                                     4 IGHLY
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APPLICANT: Luiten, Rosalie
APPLICANT: Luiten, Rosalie
APPLICANT: Luiten, Rosalie
APPLICANT: Bono-Falleur, Thierry
APPLICANT: Van der Bruggen, Pierre
APPLICANT: Schoolant, Vincent
APPLICANT: Schultz, Erwin
TITLE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44
FILE REFERENCE: L0461/7104
CURRENT APPLICATION NUMBER: US 60/177,242
FRIOR APPLICATION NUMBER: US 60/177,242
FRIOR PILING DATE: 2000-10-19
FRIOR FILING DATE: 2000-10-25
WUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 3.0
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CURREWY PAPLICATION NUMBER: US/09/909,460
CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/321,346
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Sequence 51, Application US/09909460
FOURING NO. US20020182258A1
GENERAL INFORMATION:
APPLICANT: Lunsford, Lynn B.
APPLICANT: Putnam, David
APPLICANT: Hedley, Mary Lynn
TITLE OF INVENTION:
TITLE OF INVENTION: ACID
                                                                                                                                                                                                                                                                                                       58.0%; Score 29; DB 9; Length 9; 100.0%; Pred. No. 8.9e+04; Live 0; Mismatches 0; Indels
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8.9e+04;
CURRENT APPLICATION NUMBER: US/09/766,889A;
CURRENT FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 60/177,242
PRIOR FILING DATE: 2000-01-20
PRIOR PLING DATE: 2000-11-25
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 3.0
SSEQ ID NO 18
LENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 56, Application US/09766889A ; Patent No. US20020164654A1
                                                                                                                                                                                                                                                                                                         Query Match 58.0
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 58.0
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens US-09-766-889A-56
                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-09-766-889A-18
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5 IGHLY 9
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5 IGHLY 9
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US-09-766-889A-56
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Luiten, Rosalie
APPLICANT: Boon-Falleur, Thierry
APPLICANT: Boon-Falleur, Thierry
APPLICANT: Stroobant, Vincent
APPLICANT: Stroobant, Vincent
APPLICANT: Schultz, Erwin
TITLE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B44
FILE REPRENCE: L0461/7104
CURRENT PAPLICATION NUMBER: US/09/766,889A
CURRENT PILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 60/177,242
PRIOR APPLICATION NUMBER: US 60/243,212
PRIOR FILING DATE: 2000-10-25
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 10
            TITLE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44
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                                                                                                                                                                                                                                                                                                                                    Length 10;
                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                  Query Match 58.0%; Score 29; DB 9; Best Local Similarity 100.0%; Pred. No. 4.6; Matches 5; Conservative 0; Mismatches (
                       FILE REFERENCE: LO461/7104
CURRENT APPLICATION NUMBER: US/09/766,889A
CURRENT FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 60/177,242
PRIOR FILING DATE: 2000-01-20
PRIOR FILING DATE: 2000-10-25
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 3.0
SECTION 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 59, Application US/09766889A Patent No. US20020164654A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-766-889A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens US-09-766-889A-59
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Best Local Similarity
5; Conserve
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| IGHLY 10
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6 IGHLY 10
                                                                                                                                                                                                                                                                                                                                                                                                                  4 IGHLY 8
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US-09-766-889A-59
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US-09-923-831-6
Sequence 6, Application US/09923831
Sequence 6, Application US/09923831
Fatent No. US20020115142A1
GENERAL INFORMATION:
APPLICANT: Martelange, Val.rie
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR
FILE REFERENCE: L0461/7054
CURRENT APPLICATION NUMBER: US/09/923,831
CURRENT FILING DATE: 2001-08-07
FRIOR APPLICATION NUMBER: 09/183,706
FRIOR APPLICATION NUMBER: 09/183,706
NUMBER OF SEQ ID NOS: 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
58.0%; Score 29; DB 10; L
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 5; Conservative 0; Mismatches 0;
                                                                         PRIOR APPLICATION NUMBER: 09/201,931

**PLICATION NUMBER: 09/201,931

**FILING DATE: COLMONN-
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815

**REGISTRATION INFORMATION:
TELECOMMUNICATION IMPORMATION:
TELEPHONE: (619)535-9001

TELEPHONE: (619)535-8949

INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                       APPLICATION NUMBER: US/09/847,185
                                                                                                                                                                                                                                                                                                        LENGTH: 9 amino acids
TYPE: amino acids
TYPE: amino acid
TYPE: amino acid
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
                                       FILING DATE: 01-May-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20, Application US/09766889A
Patent No. US20020164654A1
GENERAL INFORMATION:
APPLICANT: Luiten, Rosalie
APPLICANT: Boon-Falleur, Thierry
APPLICANT: van der Bruggen, Pierre
APPLICANT: Stroobant, Vincent
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Demotte, Nathalie
Schultz, Erwin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 58.0
Best Local Similarity 100.
Matches 5; Conservative
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US-09-923-831-6
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| IGHLY 9
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5 IGHLY 9
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US-09-766-889A-20
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APPLICANT:
APPLICANT:
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Gaps

us-09-692-401-5.closed.rai

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33, Appl
15, Appl
6, Appli
6, Appli
13, Appli
47, Appl
6, Appli
18, Appli
18, Appli
15, Appli
18, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BOOM, Thierry; van der Bruggen, Pierre;
APPLICANT: Be Plaen, Etienne; Lurquin Christophe; Traversari, Catia
TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM
TITLE OF INVENTION: MAGE GENES AND USES THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDESS:
ADDRESSEE: Falfe & Lynch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                       Sednence Sed
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Sequence
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US-08-880-963-18
US-08-354-679C-15
US-08-354-679C-17
US-08-159-339A-576
US-09-183-931-27
US-09-183-931-33
US-09-183-931-33
US-08-393-273E-15
US-09-162-934-3
US-09-162-48-47
US-09-166-44-47
US-09-166-44-47
US-09-567-995-6
US-09-412-928-18
US-09-413-580F-15
US-08-443-580F-17
US-08-443-580F-17
US-09-461-083-18
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Pred. No. 1.9e+05;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: MAGE-21 derived nonapeptide US-07-938-334C-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/938,334C
FILING DATE: 31-AUG-1992
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: LUD 293
TELECOMMUNICATION INFORMATION:
TELEPAN: (212) 688-9200
TELEPAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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100.0%; Pre
0; )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5405940man
REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
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Best Local Similarity
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Sequence 16,
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Sequence 1
Sequence 2
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                 GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-08-073-103A-16

US-08-443-411-16

US-08-348-679C-16

US-08-34-679C-16

US-08-34-679C-16

US-08-443-30

US-08-736-83-30

US-08-217-188A-27

US-08-217-188A-27

US-08-07-28-27

US-08-07-28-27

US-08-07-103A-17

US-08-07-103A-15

US-08-07-113A-17

US-08-07-113A-17

US-08-07-113A-17

US-08-07-113A-17

US-08-07-113A-17

US-08-07-113A-17

US-08-186-266-4

US-08-186-266-4

US-08-186-266-4

US-08-186-266-1
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US-08-498-461-10
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US-08-902-516-23
US-09-036-582-3
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Maximum Match 100%
Listing first 45 summaries
                                                                                              protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1 WWRIGHLYIL 10
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Match Length
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MAGE-3 GENE AND PRESENTED BY HLA-A1 AND USES THEREOF
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Patent No. 5827073
GENERAL INFORMATION:
APPLICANT: Luescher, Immanuel; Anjuere, Fabienee;
APPLICANT: Layer, Andreas; Romero, Pedro; Cerottini, Jean-Charles TITLE OF INVENTION: Photoreactive Peptide Derivatives
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM TITLE OF INVENTION: MAGE-3 GENE AND PRESENTED BY HLA-A. NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Diskette, 3.5 inch, 1.44 kb storage COMPUTER: IBM OPERATING SYSTEM: PC-DOS SOFTWARE: Wordperfect
                                                                                                                                                                                                              ZIF: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                               COMPUTER: 18M PS/2
COMPUTER: 18M PS/2
COMPUTER: 18M PS/2
COMPUTER: 18M PS/2
COMPUTER: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,341
FILING DATE: 17-MAY-1995
CLASSIFICATION NUMBER: 08/073,103
FILING DATE: 7-JUNE-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/938,334
FILING DATE: 31-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/938,334
FILING DATE: 31-AUG-1992
RIOR APPLICATION NUMBER: 08/037,230
FILING DATE: 26-MARCH-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LUD 5293.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Hanson, No. 5695994man D. REGISTRATION NUMBER: 30,946
REPERENCE/DOCKET NUMBER: LUD 525
TELECOMUNICATION:
TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 16:
SEGUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                  STREET: 805 Third Avenue CITY: New York City STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
                                                                                                 Felfe & Lynch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: sir
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                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-443-341-16
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US-08-498-461-15
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                                                                                                                                                          APPLICANT: Boon-Falleur, Thierry
APPLICANT: van der Bruggen, Pierre
APPLICANT: be Plaen, Etienne
APPLICANT: Lurquin, Christophe
APPLICANT: Traversari, Catia
APPLICANT: Gaugler, Beatrice
APPLICANT: Gaugler, Beatrice
APPLICANT: Gaugler, Beatrice
TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM
TITLE OF INVENTION: MagG-3 GENE AND PRESENTED BY HLA-A1 AND USES THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COPERATING SYSTEM: PC-DOS
SOSTWARE: WORDEFICED
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/073,103A
FILING DATE: 7-JUNE-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/938,334
FILING DATE: 31-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5462871man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5293.1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Boon-Falleur, Thierry
van der Bruggen, Pierre
De Plaen, Etienne
Lurquin, Christophe
Traversari, Catia
Gaugler, Beatrice
Van den Eynde, Benoit
                                                                                       Sequence 16, Application US/08073103A Patent No. 5462871 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16, Application US/08443341
Patent No. 5695994
GENERAL INFORMATION:
APPLICANT: Boon-Falleur, Thierry
APPLICANT: Van der Bruggen, Pierry
APPLICANT: De Plaen, Etienne
                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
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TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 16:
SEGUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 84.0
Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-073-103A-16
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                                                                   US-08-073-103A-16
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APPLICANT:
APPLICANT:
APPLICANT:
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Sequence 16, Application US/08393273E
Patent No. 6222012
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BOON-FALLEUR, Thierry; VAN DER BRUGGEN,
APPLICANT: PLAEN, Etienne; LURQUIN, Christophe; TRAVERSARI, Catia;
APPLICANT: GAUGLER, Beatrice; VAN DEN EYNDE, Benoit; ROMERO, Pedro TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRBY APPLICATION DATA:
APPLICATION NUMBER: US/08/393,273E
FILING DATE: 23-February-1995
          100.0%; Pred. No. 1.9e+05; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42; DB 4; Le
Pred. No. 1.9e+05;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Fulbright & Jaworski LLP
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,103
FILING DATE: 7-0une-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/938,334
FILING DATE: 31-August-1992
PRIOR APPLICATION NUMBER: 07/037,230
FILING DATE: 26-MAICH-1993
APPLICATION NUMBER: 07/037,230
FILING DATE: 26-MAICH-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6222012man D.
REGISTRATION NUMBER: 30,946
MREGISTRATION NUMBER: 1UD 5293.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
US-08-443-580F-16
: Sequence 16, Application US/08443580F
; Patent No. 6379901
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100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100...
Best Local 8; Conservative
                                  Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
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             Best Local Similarity
Matches 8; Conserv
                                                                                                1 VVRIGHLY 8
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US-08-393-273E-16
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Patent No. 6034214
GENERAL INFORMATION:
APPLICANT: Boon, Thierry: van der Bruggen, Pierre;
APPLICANT: De Plaen, Etienne; Lurquin Christophe; Traversari, Catia TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM TITLE OF INVENTION: MAGE GENES AND USES THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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0
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MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb storage
COMPUTER: LBM FS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/354,679C
FILING DATE: 13-DECEMBER-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/938,334
                                                                                                                                                                                                                                                                                                                                                                               84.0%; Score 42; DB 2; Le
100.0%; Pred. No. 1.9e+05;
Live 0; Mismatches 0;
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                                                                                                    NAME: Hanson, No. 5827073man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5403
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                     APPLICATION NUMBER: US/08/498,461
FILING DATE: 5-JULY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 07/938,334
FILING DATE: 31-AUGUST-1992
ATTORNEY/AGENT INFORMATION:
NAME: BAER, MADELINE F.
REGISTRATION NUMBER: 36,437
REFERENCE/DOCKET NUMBER: LUD 5293
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 838-9884
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
                                                                                   ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 100.
Matches 8; Conservative
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                                                          TYPE: amino acid;
TOPOLOGY: linear
US-08-498-461-15
                                         FILING DATE: 5-
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 WWRIGHLY 8
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Sequence 30, Application US/08602506A
Sequence 30, Application US/08602506A
GENERAL INFORMATION:
APPLICANT: Herman, Jean; Coulie, Pierre;
APPLICANT: Luescher, Immanuel:
TITLE OF INVENTION: Tumor Rejection Antigens Presented By HLA-
TITLE OF INVENTION: B44 Molecules, And Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42; DB 1; Length 10;
Pred. No. 0.013;
0; Mismatches 0; Indels
                                            Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diskette, 3.5 inch, 360 kb storage
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,506A
FILING DATE: 20-FEBRUARY-1996
                                                                                                                                                                                                                   PULICATION DATA:
PRIOR APPLICATION NUMBER: 08/602,506
FILING DATE: 20-FEBRUARY-1996
FILING DATE: 21-SEPTEMBER-1995
FILING DATE: 21-SEPTEMBER-1995
FILING DATE: 31-SEPTEMBER-1995
FILING DATE: 17-SEPTEMBER-1995
FILING DATE: 17-JANUARY-1995
FILING DATE: 17-JANUARY-1995
FILING DATE: 3-JUNE-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAISON, NO. 5744353man D.
REGISTRALION NUMBER: 30,946
REGISTRALION NUMBER: 30,946
                                                                                                                                                      APPLICATION NUMBER: US/08/796,883
FILING DATE: 06-FEB-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LUD 5436
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Best Local Similarity 100.0%; Pr
Matches 8; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-3200
TELEPHONE: (212) 838-3884
INFORMATION FOR SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: Mage-12/HLA-B44
US-08-796-883-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
                                                                                       OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 amino acids
                                                                                                              SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New York
                                               MEDIUM TYPE: D
COMPUTER: IBM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Ne.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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                APPLICANT: Boon-Falleur, Thierry; van der Bruggen, Pierre;
De Plaen, Etlenne; Lurquin Christophe; Traversari, Catia
Gaugler, Beatrice; Van den Eynde, Benoit
TITLE OF INVENTION: Method For Screening For Cancer
Using Binders For MAGE Related Peptides And Complexes
Of The Peptide And HLA Molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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Patent No. 5744353
GENERAL INFORMATION:
APPLICANT: Herman, Jean; Coulie, Pierre;
APPLICANT: Herman, Jean; Coulie, Pierre;
APPLICANT: Luescher, Immanuel.
TITLE OF INVENTION: Tumor Rejection Antigens Presented By
TITLE OF INVENTION: HLA-B44 Molecules, And Uses Thereof
NUMBER OF SEQUENCES: 30
                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P. STREET: 666 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM, PH.D./2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,580F
FILING DATE: 17-May 1995
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: 08/073,103
APPLICATION NUMBER: 08/073,103
APPLICATION NUMBER: 07/938,334
FILING DATE: 31-MGUST-1992
APPLICATION NUMBER: 08/037,230
FILING DATE: 26-MARCH-1993
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Hanson, NO. 6379901man D. REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5293.4
TELECOMMUICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFROME: (212) 752-5958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
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100.0%; Pred
0; N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (212) 752-5
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                CITY: New York City STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                  ZIP: 10103
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 84.0
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 3C
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Ly
                                                                                                                                                                                                                                                                                            USA
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GENERAL INFORMATION:
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STATE:
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APPLICANT: Wallet, Cornelis J. M.; Visseren, M. W.;
APPLICANT: wan der Burg, Sjoerd; van der Bruggen, Pierre;
APPLICANT: woon Falleur, Thierry
TITLE OF INVENTION: Isolated Peptides Derived From
TITLE OF INVENTION: MAGE-2, Cytolytic T Cells Specific To Complexes Of
TITLE OF INVENTION: Peptides And HLA-A2 Molecules, And Uses Thereof
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
                                                                                                                                                                                                   Length 9;
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                                                                                                                                                                                                   Score 31; DB 1; 1
Pred. No. 1.9e+05;
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                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/687,226
FILING DATE: 25-ULX-1996
CLASSIPICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LUD 5447
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US-08-667-725B-27
: Sequence 27, Application US/08667725B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 27, Application US/08687226. Patent No. 5686068
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Hanson, No. 5686068man D. REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/217,188
FILING DATE: 24-MARCH-1994
ATTORNEY/AGENT INFORMATION:
                  LENGTH: 9 amino acid residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 amino acid residues
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LET ROS Third Avenue
New York City
New York
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TELEPHONE: (112) 688-9200
TELEPAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
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85.7%;
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                                                                                                                                                                Query Match
Best Local Similarity 85./v
Best Local 6; Conservative
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Best Local Similarity 85.7<sup>,</sup>
Lange 6; Conservative
                                               ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-217-188A-27
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2 ISHLYIL 8
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US-08-687-226-27
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Patent No. 5554724
GENERAL INFORMATION
APPLICANT: Melief, Cornelis J. M.
APPLICANT: Visseren, M. J. W.
APPLICANT: Rast, W. M.
APPLICANT: Boon-Falleur, Thierry
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Tumor Rejection Antigen
TITLE OF INVENTION: Precursor MAGE-2 Derived Peptides, and Uses Thereof CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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100.0%; Pred. No. 0.013;
Live 0; Mismatches 0; Indels
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MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Wordperfect
CURRENT APPLICATION DAIR:
APPLICATION NUMBER: US/08/217,188A
FILING DATE: 24 WARCH-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFO MAN ATTORNEY AGENT INFO MAN ATTORNEY AGENT INFO MAN ATTORNEY AGENT INFO MAN ATTORNEY ATTORNEY AND ATTORNEY AT
                         APPLICATION NUMBER: 08/531,864
FILING DATE: 21 SEPTEMBER-1995
PHOR APPLICATION DATA: 33,636
FILING DATE: 17-JANUARY-1995
FILING DATE: 17-JANUARY-1995
APPLICATION NUMBER: 08/253,503
FILING DATE: 3-JUNE-1994
ATTORNEY/AGENT INFORMATION:
REGISTRATION NOW 6060257man D.
REGISTRATION NOW 6060257man D.
REGISTRATION NOW 6060257man D.
REGISTRATION NOW 6060257man D.
                                                                                                                                                                                                                                                                                                                                                                       LUD 5436
                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: LUD TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 688-9200 TELEFAX: (212) 838-384 INFORMATION FOR SEQ ID NO: 30: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: Mage-12/HLA-B44
US-08-602-506A-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 8; Conservative
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
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Sequence 2, Application US/07938334C

Patent No. 5405940

GENERAL INFORMATION:
APPLICANT: Boon, Thierry; van der Bruggen, Pierre;
APPLICANT: Boon, Thierry; van der Bruggen, Pierre;
APPLICANT: De Plaen, Etienne; Lurquin Christophe; Traversari, Catia
TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM
TITLE OF INVENTION: MAGE GENES AND USES THEREOF
NUMBER OF SEQUENCES: 22
CORRESSONDENCE ADDRESS:
ADDRESSEDE: Felfe & Lynch
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage COMPUTER: IBM PS/COMPUTER: TBM PS/COMPUTER: GORDANING SYSTEM: PC-DOS SOFTWARE: Wordperfect SOFTWARE: Wordperfect APPLICATION DATA:
APPLICATION NUMBER: US/O7/938,334C
FILING DATE: 31-AUG-1992
                                                                                                                                                                                        LUD 5340.2 DIV (081572)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 31; DB 4;
Pred. No. 1.9e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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SOFTWARE: Wordperfect
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/007,748
FILING DATE: 15 January 1998
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 614/187man D.
REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5405940man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 293
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 9 amino acid residues
                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: LI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEO ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.0%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 62.0
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 805 Third Av
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 IGHLYIL 10
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2 ISHLYIL 8
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US-07-938-334C-2
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APPLICANT: Melief, Cornelis J. M.
APPLICANT: Walseren, M. J. W.
APPLICANT: Vasseren, M. M.
APPLICANT: van der Bruggen, Pierre
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Tumor Rejection Antigen
TITLE OF INVENTION: Precursor MAGE-2 Derived Peptides, and Uses Thereof
                                                 APPLICANT: Visseren, M. J. W.
APPLICANT: Kast; W. M.
APPLICANT: van der Brugen, Pierre
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Tumor Rejection Antigen
TITLE OF INVENTION: Precursor MAGE-2 Derived Peptides, and Uses Thereof
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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Pred. No. 1.9e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                COUNTAL
21P: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6063900man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5340.1 DIV (081585)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 752-5958
INFORMATION FOR SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Fulbright & Jaworski LLP
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                ADDRESSEE: Fulbright & Jaworski LLP
STREFF: 66 Fifth Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/667,725B
FILING DATE: 21 June 1996
CLASSIFICATION: 530
                              APPLICANT: Melief, Cornelis J. M. APPLICANT: Visseren, M. J. W. APPLICANT: Kast; W. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 27, Application US/09007748 Patent No. 6147187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acid residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.0%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 62.0
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
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MEDIUM TYPE: Diskette
COMPUTER: IBM PS/2
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CORRESPONDENCE ADDRESS:
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              GENERAL INFORMATION:
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2 ISHLYIL 8
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US-09-007-748-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/07938334C
Fatent No. 5405940
GENERAL INFORMATION:
APPLICANT: Boon, Thierry; van der Bruggen, Pierre;
TITLE OF INVENTION: SOLATED NONAPERTIDES DERIVED FROM
TITLE OF INVENTION: MAGE GENES AND USES THEREOF
OWNBER OF SEQUENCES:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITT: New York City
COUNTRY: USA
                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Query Match

Se.0%; Score 29; DB 1; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 6; Conservative 0; Mismatches 2; Indels
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MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage COMPUTER: Diskette, 5.25 inch, 360 kb storage COMPUTER: Diskette, 5.25 inch, 360 kb storage SOFTWARE: Wordperfect

COMPUTER: Diskette, 5.25 inch, 360 kb storage SOFTWARE: Nordperfect

COMPUTER: Diskette, 5.25 inch, 360 kb storage

COMPUTER: DISKETE INCH TOOR

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein FEATURE:
                                                                                                                                                                                                1 VVRIGHLY 8
                                                                                                                                                                                                                                                       4 IGHLY 8
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5 IGHLY 9
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US-07-938-334C-4
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Search completed: December 19, 2002, 16:52:37 Job time : 33 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

December 19, 2002, 16:49:09; Search time 15 Seconds (without alignments) 64.090 Million cell updates/sec

US-09-692-401-5 50 1 VVRIGHLYIL 10 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 283224 seqs, 96134422 residues Searched:

1100

Minimum DB seq length: 0 Maximum DB seq length: 10

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_73:\* 1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	· Description	rel - Caibemornen	י ט כ	) (F	2	ď	2	- Au	D-amino-acid oxida	qluconokinase (EC		cardioexcitatory n	e antigen p20e pre	leucosulfakinin II	neomyosuppressin -	carbon-monoxide de		Iq heavy chain CRD	cytochrome-c oxida	glyceraldehyde-3-p	growth-modulating	sarcosine dehydrod	collagen alpha 1(I	hypothalamic hepta	gramicidin S svnth	•	Roh	pai	erythrocyte membra	T-cell receptor be
SUMMARIES	O.	PO0177	A60647	A59173	A30823	138888	S07205	S07204	S39437	S74176	GMROL2	A32543	B46453	B60656	A56633	PL0140	A28709	PT0238	T14212	S74147	GKHU	A61419	B56979	NYPG7	S42407	A61467	S07241	A61289	XGHUE	PT0721
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o¥.	Query Match	42.0	42.0	40.0	38.0	34.0	34.0	34.0	34.0	34.0	32.0	32.0	32.0	32.0	32.0	30.0	30.0	30.0	30.0	30.0	28.0	28.0	28.0	28.0	28.0	28.0	28.0	28.0	28.0	26.0
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	Result No.	1	7	m	4	Ŋ	9	7	ω (	on (	10	11	12	13	14	15	16	17	18	19	707	21	7.7	23	24	25	<b>5</b> 6	27	28	29

fatty-acid synthas membrane protein - sex pheromone cAM3 hypothetical L2 pr ribosomal protein virG protein - Agr hypothetical prote cytochrome-coxida monodehydroascotha gamma subunit of P N-formyl oligopept microcin C7 - Esch serum albumin - do telomeric and tetr coat protein beta	ALIGNMENTS	RESULT 1 PQ0177 neurcomedin C - laughing frog neurcomedin C - laughing frog C; Species: Rana ridibunda (laughing frog) C; Accession: PQ0177 R; Conlon, J.M.; O'Harte, F.; Vaudry, H. Biochem. Biophys. Res. Commun. 178, 556-530, 1991 A; Title: Primary structures of the bombesin-like neuropeptides in frog brain show tha A; Reference number: PQ0177; MUID:91315477; PMID:1859413 A; Accession: PQ0177 A; Molecule type: protein A; Residues: 1-10 <con> A; Accession: PQ0177 A; Molecule type: protein A; Residues: 1-10 <con> A; Experimental source: brain C; Superfamily: gastrin-releasing peptide C; Superfamily: gastrin-releasing peptide C; Superfamily: gastrin-releasing peptide C; Superfamily is dastrin-releasing peptide</con></con>	1. 21; DB 2; Length 10;
A60139 P20263 P20269 156695 S78420 S06324 A142312 A142313 A448360 A6030	ALIG	ng frog islon 2 IX, H. IX, 556- ee bombe 9131547 peptide	Score
000400000000000000		log carb	.; ee ee
77777777777777777777777777777777777777		C - laughing frog Rana ridibunda (lau Nov-1991 #sequence: PQ0177 O'Harte, F.; V. OPhys. Res. Commun. imary structures of .: number: PQ0177; MI .: PQ0177; MI .: PQ180177 .: PQ180177 .: PQ180177; MI .:	42.0%;
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		RESULT 1  PQ0177  neuromedin C - laughing frog  C; Species: Rana ridibunda (laughing fro  C; Date: 23-Nov-1991 #sequence_revision  C; Accession: PQ0177  R; Conlon, J.M., O'Harte, F.; Vaudry, H.  Biochem. Blophys. Res. Commun. 178, 526  A; Title: Primary structures of the bomb  A; Reference number: PQ0177; MUID:913154  A; Molecule type: protein  A; Residues: 1-10 <con>  A; Residues: 1-10 <con>  A; Reperimental source: brain  C; Superfamily: gastrin-releasing peptid  C; Keywords: amidated carboxyl en  F; 10/Modified site: amidated carboxyl e</con></con>	Query Match Best Local Similarity
00000000000000000000000000000000000000		RESULT 1 PQ0177 C. Species: C. Species: C. Accession R. Conlon, B. M. Title: Pr A. Reference A. Accession A. Medecasion A. Residues C. Superimen C. Superimen C. Superimen C. Superimen C. Keywords: F. 10/Modifile	Query Best I

RESULT 2
A66647
neuromedin C - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 07-May-1999
C:Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 07-May-1999
C:Accession: A60647
R:Lemaire, S: Trifaro, J.M.; Chouinard, L.; Cecyre, D.; Dessureault, J.; Mercier, P. Peptides 10, 355-360, 1989
A:Title: Structural identification, subcellular localization and secretion of bovine A:Reference number: A60647; MUID:89331342; PMID:2755876
A:Mocession: A60647
A:Molecule type: protein
A:Molecule type: protein
A:Molecule type: protein
A:Molecule type: protein
C:Superfamily: gastrin-releasing peptide
C:Superfamily: agatrin-releasing peptide
C:Keywords: adrenal gland; neuropeptide ö ö Gaps Gaps ; 0 . 0 Query Match
42.0%; Score 21; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 4.1e+02;
Matches 3; Conservative 1; Mismatches 0; Indels Indels Best Local Similarity 75.0%; Pred. No. 4.1e+02;
Matches 3; Conservative 1; Mismatches 0; :||| 6 VGHL 9 4 IGHL 7 :||| VGHL 9 4 IGHL 7 Ωp δλ g δy

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Decides (fragment)

C; Species: Trigonopsis variabilis
C; Species: Trigonopsis variabilis
C; Species: Trigonopsis variabilis
C; Species: Trigonopsis variabilis
C; Species: 19 Mar-1997 #sequence_revision 05-Dec-1997 #text_change 07-May-1999
C; Accession: S33437
R; Schraeder, T.; Andreesen, J.R.
R; Reference number: S39437; MUID:94094869; PMID:7903639
R; Residues: 1-9 <SCH>
R; Residues: 1-9 <SCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             litorin I - Australian tree frog (Litoria aurea)
C;Species: Litoria aurea
C;Species: Litoria aurea
C;Species: Litoria aurea
C;Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 18-Aug-2000
C;Accession: S07204
R;Anastasi, A.; Erspamer, V.; Endean, R.
Experientia 31, 510-511, 1975
A;Title: Aminoacid composition and sequence of litorin, a bombesin-like nonapeptide fareference number: S07204; MUID:7518/011; PMID:1140241
A;Accession: S07204
                                                                                                                                                                                                                                                                                                 Cydroession: S07205
RyAnastasi, A.; Montecucchi, P.; Angelucci, F.; Erspamer, V.; Endean, R. Exparientia 33, 1289, 1977
RyTitle: Glu(OMe)(2)-11torin, the second bombesin-like peptide occurring in methanol A; Reference number: S07205; MUD:78003546; PMID:908397
A; Molecule type: protein
A; Residues: 1-9 <ANA>
C; Superfamily: gastrin-releasing peptide
C; Superfamily: gastrin-releasing peptide
F; J,Modified site: pyrrolidone carboxyl end; neuropeptide; pyroglutamic acid
F; J,Modified site: amidated carboxyl end (Met) #status experimental
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                                                                                                                                                                                                                                             C;Species: Litoria aurea
C;Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 18-Aug-2000
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A, Residues: 1-9 <ANA>
C, Superfamily: qastrin-releasing peptide
C, Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F, 1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F; 9/Modified site: amidated carboxyl end (Met) #status experimental
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                                                                                                                                                                                                                   litorin 2-Glu - Australian tree frog (Litoria aurea)
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66.7%;
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Best Local Similarity 66.7
Matches 2; Conservative
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Best Local Similarity
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QLGH 4
3 RIGH 6
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C:Species microhondrion Podospora anserina
C:Date: 03-Peb-1994 #sequence_revision 03-Feb-1994 #text_change 07-Dec-1999
C:Accession: 13888
S:Cummings, D.J.; Michel, F.; McNally, K.L.
Curr. Genet. 16, 381-406, 1899
A.Title: DNA sequence analysis of the 24.5 kilobase pair cytochrome oxidase subunit I mi
A.Reference number: A48327; MUID:90124722; PMID:2558809
A.Status: preliminary
A.Status: preliminary
                                                       nuclease Bhl (EC 3.1...) - Basidiobolus haptosporus (fragment)
C;Species: Basidiobolus haptosporus
C;Species: Basidiobolus haptosporus
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
C;Accession: A59173
R;Desai, N.; Shankar, V.
R;Desai, N.; Shankar, V.
R;Description: Single-strand-specific, guanylic acid preferential nuclease from Basidiok
A;Reference number: A59173
A;Reference number: A59173
A;Reference number: preliminary
A;Molecule type: protein
A;Residues: 1-10 CDES>
A;Residues: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: A30823
R;Honsi-Brandeburgo, M.I.; Queiroz, L.S.; Santo-Neto, H.; Rodrigues-Simioni, L.; Giglio, Poxicon 26, 615-627, 1988
A;Title: Fractionation of Bothrops jararacussu snake venom: partial chemical characteriz A;Reference number: A30823; MUID:89020120; PMID:3176051
A;Accession: A30823
A;Rodecule type: protein
A;Residues: I-10 <HOM>
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C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 18-Jun-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 2.8e+05;
2; Mismatches 0; Indels
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Pred. No. 6.5e+02;
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A;Residues: 1-4 <CUM>
A;Cross-references: GB:X55026; GB:M30937; GB:M61734
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Pred. No. 1e+03;
3; Mismatches
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50.0%;
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33.3%;
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Best Local Similarity 33.33
Matches 2; Conservative
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Best Local Similarity 50.0
Matches 2; Conservative
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A,Genetic code: SGC3
C,Keywords: mitochondrion
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Best Local Similarity
Matches 3; Conserv
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4 LGHL 7
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1; Conservative
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Best Local Similarity
Matches 1; Conserv
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Best Local Si
Matches 2,
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B60656
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C; Species: Leucophaea maderae (Madeira cockroach)
C; Species: Leucophaea maderae (Madeira cockroach)
C; Species: Leucophaea maderae (Madeira cockroach)
C; Stacession: Az6335
R; Nachman, R.J; Holman, G.M.; Cook, B.J.; Haddon, W.F.; Ling, N.
Biochem Biophys. Res. Commun. 140, 357-364, 1986
A; Title: Leucosulfakinin-II, a blocked sulfated insect neuropeptide with homology to chc A; Reference number: Az6335; MUID:87048769; PMID:3778455
A; Molecule type: protein
A; Residues: 1-10 < NAC;
C; Comment: This peptide was isolated from head extracts. It stimulates muscle contractic C; Superfamily: gastrin
C; Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid; sulfoprotein
F; 1/Modified site: pyrrolidone carboxyl end (Phe) #status experimental
F; 10/Modified site: sulfate (Tyr) (covalent) #status experimental
F; 10/Modified site: amidated carboxyl end (Phe) #status experimental
A;Experimental source: CBS 4095
C;Function:
A;Description: oxidoreductase; catalyzes the oxidation of D-amino acids to their corresp
A;Note: reoxidation of the enzyme by molecular oxygen is accompanied by the release of H
C;Keywords: FAD; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rizu, H.; Adachi, O.; Yamada, M.
FEBS Lett. 394, 14-16, 1996
A;Title: Purification and characterization of the Escherichia coli thermoresistant glucd
A;Reference number: S74176; MUID:97074194; PMID:8925917
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                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 2.6e+03;
1; Mismatches 0;
                                                                                                                                                                                                                                 Score 17; DB 2; Dred. No. 2.8e+05; Dred. No. 2.8e+05; Dred. No. 2.8e+05; No. 2.8e+06; No. 2.8e+0
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C;Keywords: dimer; phosphotransferase
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A,Residues: 1-10 <IZU>
A,Experimental source: strain K-12
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66.7%;
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66.7%;
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Best Local Similarity 66./.
2; Conservative
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Best Local Similarity
Matches 2; Conserv
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RESULT 11

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cardioexcitatory neuropeptide - desert locust
C;Species: Schistocerca gregaria (desert locust)
C;Date: 20-Dec-1989 #sequence_revision 20-Dec-1989 #text_change 18-Aug-2000
C;Accession: A32543
R;Robb, S.; Packman, L.C.; Evans, P.D.
Biochem: Biophys. Res. Commun. 160, 850-856, 1989
A;Title: Isolation, primary structure and bioactivity of SchistoFLRf-amide, a FWRF-am A;Reference number: A32543
A;Accession: A32543
A;Stelliminary
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N;Alternate names: HBe antigen
N;Contains: entigen
C;Species: hepatitis B virus, HBV
A;Variety: subtype adr
C;Date: 18-Jun-1993 #sequence_revision 08-Nov-1996 #text_change 15-Aug-1997
C;Accession: B46451; Kishimoto, S.; Ohori, K.; Yoshizawa, H.; Machida, A.; Ohnuma, H.; Ts
J:Immunol. 147, 3156-3160, 1991
A;Title: Molecular heterogeneity of e antigen polypeptides in sera from carriers of h
A;Reference number: A46453; MUID:92013147; PMID:1717588
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A:Accession: B60656; MUID:90137190; PMID:2615921
A:Accession: B60656
A:Accession: B
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Cispecies: Periplaneta americana (American cockroach)
Cibate: 14 May-1993 #sequence_revision 14-May-1993 #text_change 08-Dec-1995
Cisccession: B60656
Riveenstra, J.A.
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A; Residues: 1-10 <ROB>
C; Superfamily: unassigned animal peptides
C; Keywords: amidated carboxyl end; neuropeptide
F; 10/Modified site: amidated carboxyl end (Phe) #status experimental
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A;Note: sequence extracted from NCBI backbone (NCBIP:60243)
F;1-10/Domain: signal sequence (fragment) #status predicted <SIG>
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22.2%; Pred. No. *..
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Carbon monoxide dehydrogenase (EC 1.2.99.2) large chain - Pseudomonas carboxydohydrogena carbon-monoxide dehydrogenas carboxydohydrogena c.; Species: Pseudomonas carboxydohydrogena C; Species: Pseudomonas carboxydohydrogena C; Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Apr-1993 C; Accession: PLO140
R:Kraut, M.; Hugendieck, I.; Herwig, S.; Meyer, O. Arch. Microbiol. 152, 335-341, 1989
A.Tille: Homology and distribution of CO dehydrogenase structural genes in carboxydotrop A; Reference number: PLO138; MUID:90055678; PMID:2818128
A.Accession: PLO140
A.Accession: PLO140
A.Accession: PLO140
A.Accession: L4 «KRA»
C; Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large, me C; Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                            C; Species: Sarcophaga bullata
C; Species: Sarcophaga bullata
C; Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 20-Jun-2000
C; Accession: A56633
R; Fonagy, A.; Schoofs, L.; Proost, P.; Van Damme, J.; Bueds, H.; De Loof, A.
Comp. Biochem. Physiol. C 102, 239-245, 1992
A; Title: Isolation, primary structure and synthesis of neomyosuppressin, a myoinhibiting A; Reference number: A56633; MUID:93047886; PMID:1358537
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N.Alternate_names: Neb-MS
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GenCore version 5.1.3
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OM protein - protein search, using sw model

December 19, 2002, 16:46:03; Search time 10 Seconds (without alignments) 41.476 Million cell updates/sec Run on:

US-09-692-401-5 50 1 VVRIGHLYIL 10 Title: Perfect score: Sequence:

Scoring table:

112892 seqs, 41476328 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

346 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 10

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID		LITO_LITAU	NEUX_HUMAN	NSK1_SARBU	FARP_LOCMI	LCMS_LEUMA	LSK2_LEUMA	NEMS_DROME	DCML_PSECH	GRWM_HUMAN	FAR2_ASCSU	HY7_PIG	LITR_PHYRO	GLEM_HUMAN	CIA_ENTFA	GFRP_MOUSE	PGLR_DIAAB	ANG2_BOTJA	MOSH_CLYJA	RE42_LITRU	RS10_SERMA	ANGT_BOVIN	FARP_ARTTR	PSK_DAUCA	UN06_PINPS	ALL6_CYDPO	CONO_CONST	ISOT_CYPCA	NEUU_CAVPO	OXYA_SCYCA	OXYA_SQUAC	OXYT_BUFRE	OXYT_CYPCA
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0 9 1 OXYT_RABIT 0 9 1 OXYT_RAJCL 0 1 OXYY_SQUAC 10 1 ANGI_BOTJA 0 10 1 FARP_MANSE 10 1 FARP_MANSE 10 1 UPAS_HUMAN 10 1 UPAS_HUMAN 10 1 UXA6_CHLTR 0 5 1 TPIS_CANFA 6 1 FARP_MOSE 6 1 FARP_MOSE 6 1 FARP_MOSE	4 (180 (OS) E Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z	TANDARD; PRT;  09, Created)  28, Last sequence to the contraction and golden bell oa; Chordata; Craniat Anura; Neobatractionia.  PubMed=1140241;
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                                                                  SEQUENCE (METHYLATED VARIANT).
MEDLINE-78003546; Pubmed-908397;
Anastasi A., Montecucchi P.C., Angelucci F., Erspamer V., Endean R.;
"Glu(OMe) 3-litorin, the second bombesin-like peptide occurring in
methanol extracts of the skin of the Australian frog Litoria aurea.";
Experientia 33:1289-1289(1977).
- SUBCELLULAR LOCATION: Secreted.
- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The amino acid sequence of kinetensin, a novel peptide isolated from pepsin-treated human plasma: homology with human serum albumin, neurotensin and angiotensin.";
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606, 9913, 9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES-Human, Bovine, and Rabbit;
MEDLINE=8194805; PubMed-2437111;
Carraway R.E. Mitra S.P., Cochrane D.E.;
Structure of a biologically active neurotensin-related peptide obtained from pepsin-treated albumin(s).";
J. Biol. Chem. 262-25968-5973(1987).
-: FUNCTION: REGULATION OF FAT DIGESTION, LIPID ABSORPTION, AND BLOOD FLOW (POTENTIAL).
PIE, A03229; ABHUSK.
PIR; A26693; A26693.
           "Aminoacid composition and sequence of litorin, a bombesin-like nonapeptide from the skin of the Australian leptodactylid frog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES=Human;
MEDLINE=86242180; PubMed=3087352;
Mogard M.H., Kobayashi R., Chen C.F., Lee T.D., Reeve J.R. Jr.,
Shively J.E., Walsh J.H.;
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D7CC1E862CDC366 CRC64;
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                                                                                                                                                                                                                                                                                                      Score 17; DB 1; Pred. No. 1.1e+05; 1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAR-1987 (Rel. 04, Created)
20-MAR-1987 (Rel. 04, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Neurotensin-related peptide (NRP) (Kinetensin)
                                                                                                                                                                                                                                                                                                                                                                                                                                    9 AA.
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PIR; S07205; S07205.

InterPro; IRR000874; Bombesin.

Pfam; PF02044; Bombesin; 1.

PROSITE; PS00257; BOMBESIN; 1.

Bombesin family; Amidation; Methylation.

MOD_RES
Endean R.;
                                             Experientia 31:510-511(1975).
                                                                                                                                                                                                                                                                                                       34.0%;
66.7%;
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 Anastasi A., Erspamer V.,
                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fondy A., Schods L., Proost P., van Damme J., de Loof A.;
Fondy A., Schods L., Proost P., van Damme J., de Loof A.;
"Isolation and primary structure of two sulfakinin-like peptides from the fleshfly, Neobellieria bullata.";
Comp. Biochem. Physiol. 103C:135-142(1992).
-!- FUNCTION: MYOTROPIC PEPTIDE.
-!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
InterPro; IPRO01651; Gastrin.
PROSITE; PS00259; GASTRIN; 1.
Neuropeptide; Amidation; Sulfation.
                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-REB-1996 (Rel. 33, Last annotation update)
01-REB-1996 (Rel. 33, Last annotation update)
Neosulfakinin-I (NEB-SK-I)
Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
NUSCOMOTPhA; Oestroidea; Sarcophagidae; Sarcophaga.
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01-0CT-1994 (Rel. 30, Last sequence update)
30-MAY-2000 (Rel. 30, Last annotation update)
SchistoFLRFamide (PDVDHELRF-amide) (Cadioexcitatory neuropeptide).
Locusta migratoria (Migratory locust), and
Schistocerca gregaria (Desert locust).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 16; DB 1; Length 9;
Pred. No. 1.18+05;
1; Mismatches 0; Indels
                     Length 9;
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8B0A0691E86B5AAA CRC64;
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Pred. No. 1.1e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 AA.
                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                              PRT;
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                     32.0%;
60.0%;
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66.7%;
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                                                                                  Conservative
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Query Match
Best Local Similarity
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0
                                                                                                                                                                            Biochem. Biophys. Res. Commun. 160:850-856(1989).

-!- FUNCTION: MUSCLE INHIBITING AGENT. INVOLVED IN THE NEURAL CONTROL OF THE VISCERAL MUSCLES OF THE HEART, ACCESSORY GLANDS AND OVIDUCT. MAY BE INVOLVED IN THE REGULATION OF SALIVA SECRETION.
-!- TISSUE SPECIFICITY: FOUND IN AXONS OF THE MALE ACCESSORY GLANDS, THE SALIVARY GLANDS, THE HEART, AND THE OVIDUCT.
-!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Hexapoda,
Insecta, Pteryota, Neoptera, Orthopteroidea, Dictyoptera, Blattaria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Holman G.M., Cook B.J., Nachman R.J.;
"Isolation, primary structure and synthesis of leucomyosuppressin, an insect neuropeptide that inhibits spontaneous contractions of the cockroach hindgut.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                          SPECIES-S.gregaria; TISSUE=Thoracic nervous system;
BODILNE-89246643; PubMed=2719702;
Robb S., Packman L.C., Evans P.D.;
"Isolation, primary structure and bioactivity of schistofirf-amide,
FMRR-amide-like neuropeptide from the locust, Schistocerca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Comp. Biochem. Physiol. 85C:329-333(1986).
-1- FUNCTION: INHIBITS THE SPONTANEOUS CONTRACTIONS OF COCKROACH
PROTODEUM (HINDGUT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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Pred. No. 1.8e+03;
4; Mismatches 1; Indels
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Pred. No. 1.8e+03;
4; Mismatches 1; Indels
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D3C51729D2C1EAB2 CRC64;
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D3C45229D2C1EAB2 CRC64;
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01-MAY-1991 (Rel. 18, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leucomyosuppressin (LMS) (LeM-MS).
Leucophaea maderae (Madeira cockroach).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blaberidae; Leucophaea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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1D LSK2_LEUMA STANDARD;

AC P09039;

DT 01-NOV-1988 (Rel. 09, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                         32.0%;
16.7%;
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16.7%;
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10 AA; 1275 MW;
Peptides 14:409-421(1993).
                                                                                                                                                                                                                                                                                                                                                          Neuropeptide; Amidation.
MOD_RES 10 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Conservative
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Best Local Similarity
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3 VDHVFL 8
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                                                                                                                                                                                                                                                                                                                         FAMILY
                                                                                                                                                               gregaria.
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SEQUENCE
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LCMS_LEDUAL

AC P21144

DT 01-FRB

DT 01-FRB

DE LEUCOMO

OC EUKATY

OC INSECT

OX NOBL_T

RR 1155UB

RR 1155UB

RR 1155UB

RR 1155UB

RR 1155UB

RR 1150UB

RR 115
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                                                                                              Periplaneta americana (American cockróach).
Eukaryota, Metazoa, Arthropoda, Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blaberoidea; Blaberidae; Leucophaea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES-L.maderae;
MEDLINE-87048769; PubMed-3778455;
Nachman R.J., Holman G.M., Cook B.J., Haddon W.F., Ling N.;
Leucosoulfakinin-II, a blocked sulfated insect neuropeptide with homology to cholecystokinin and gastrin.";
Biochem. Biophys. Res. Commun. 140:357-364(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NI TON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PYRROLIDONE CARBOXYLIC ACID. SULFATION (IN L.MADERAE, BUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9B4F5391E86B5AAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 16; DB 1; Pred. No. 1.8e+03;
01-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
10-LOCOSULEAkinin-II (LSR-II).
Leucophaea maderae (Madeira cockroach), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES=P.americana; TISSUE=Corpora cardiaca;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DOMYOSUPPPESSIN (NeomyOsuppressin) (NEB-MS).
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MEDLINE=93002195; PubMed=1390001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90137190; PubMed=2615921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001651; Gastrin.
PROSITE; PS00259; GASTRIN; 1.
Hormone; Amidation; Sulfation.
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66.7%;
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                                                                                                                                                                                                 NCBI_TaxID=6988, 6978;
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PIR; B60656; B60656.
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NCBI_TaxID=9606;
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                                                 SEQUENCE.
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P01153;
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HY7_PIG
ID HY7_P1
AC P01153
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SPECIES-S.bullata; TISSUE-Head;
MEDLINE-93047886; PubMed-1358537;
Fonagy A., Schoofs L., Proost P., Van Damme J., Bueds H., De Loof A.;
"Isolation, primary structure and synthesis of neomyosuppressin, a myoinhibiting neuropeptide from the grey fleshfly, Neobellieria bullata.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acceptor.
--- COFACTOR: Molybdenum (molybdopterin).
--- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            carboxydotrophic bacteria.";
Arch. Microbiol. 152:335-341(1989).
-!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-90055678; PubMed-2818128;
Kraut M., Hugendieck I., Herwig S., Meyer O.;
"Homology and distribution of CO dehydrogenase structural genes in
                                                                                                                                                                                                                                                                                                                                                  Pseudomonas carboxydohydrogena.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -:- CATALYTIC ACTIVITY: C0 + H(2)0 + acceptor = C0(2) + reduced
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0
                                                                                                                                                                                                                                                                                 0.1-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO dehydrogenase subunit L) (CO-DH L) (Fragment).
                                                                                                                                            Score 16; DB 1; Length 10;
Pred. No. 1.8e+03;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                AMIDATION.
D3C00329D2C1EAB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 AA; 441 MW; 7761E876F000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 15; DB 1; Le
Pred. No. 1.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 AA.
                                                                    Comp. Biochem. Physiol. 102C:239-245(1992).
-!- FUNCTION: MYOINHIBITING NEUROPEPTIDE.
Flybase; FBqn0011581; Dms.
Neuropeptide; Amidation.
MOD_RES.
10 10 AMIDATION.
                                                                                                                                                                    4; Mismatches
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                                                                                                                                                                                                                                                                 PRT;
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21-JUL-1986 (Rel. 01, Last seque
21-JUL-1986 (Rel. 01, Last anno
Growth-modulating peptide.
HOMO Sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.0%;
illarity 66.7%;
Conservative 1
                                                                                                                         10 AA; 1248 MW;
                                                                                                                                               32.0%;
                                                                                                                                                         16.78;
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                                                                                                                                                                    1; Conservative
                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                       Bradyrhizobium group.
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                                                                                                                                                         Local Similarity
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                                                                                                                                                                                        4 IGHLYI 9
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3 VDHVFL 8
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1 MGH 3
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                                                                                                                         SEQUENCE
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DCML_PSECH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ascaris suum (Pig roundworm) (Ascaris lumbricoides), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 14; DB 1; Length 7; Pred. No. 1.1e+05; 1; Mismatches 1; Indels
                                                                                                                                                                         PIR; MO1421; GKHU.
SEQUENCE 3 AA; 340 MW; 6331E8100000000 CRC64;
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SEQUENCE 7 AA; 992 MW; 69D4073B5B11E350 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-EBB-1996 (Rel. 33, Last annotation update)
FMRFamide-like neuropeptide AF2.
                                                                                                                                                                                                                                                                                                                                                                                                                 7 AA.
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MEDLINE=93324431; PubMed=8332542;
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Best Local Similarity 50.0%;
Matches 2; Conservative
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NCBI_TaxID=6253, 6233;
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nes 2; Conserv
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NCBI_TaxID=9606;
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CIA_ENTFA
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Erspamer V.;
"Rohdei-litorin: a new peptide from the skin of Phyllomedusa rohdei.";
FEBS Lett. 182:53-56(1985).
-1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                SEQUENCE, AND SYNTHESIS.
MEDLINE-81213980; PubMed-6263778;
MEDLINE-81213980; PubMed-6263778;
Chang R.C.C., Huang W.-Y., Arimura A., Redding T.W., Coy D.H.,
Saffran M., Kong A., Hanilton J.W., Cohn D.V., Schally A.V.;
"Isolation, structure and synthesis of a heptapeptide with in vitro
ACTH-releasing activity from porcine hypothalamus.";
PIR; A01417; NYPG7.
SEQUENCE 7 AA; 957 MW; 632B45B1FB5059A0 CRC64;
                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                              Phyllomedusa rohdei (Rohde's leaf frog).
Wararyota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
Phyllomedusinae; Phyllomedusa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMIDATION.
4 ECCC1E861ADC377 CRC64;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last annotation update)
Hypothalamic heptapeptide.
                                                                                                                                                                                                                                                                                                                                                    01-NOV-1988 (Rel. 09, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
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InterPro; IPR000874; Bombesin.
Pfam; PF02044; Bombesin.
PROSITE; ES00257; BOMBESIN; 1.
Bombesin family; Amidation.
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Best Local Similarity 60.00,
Best Local Similarity 3; Conservative
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nes 2; Conserv
                                                Sus scrofa (Pig).
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P02728;
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P08946;
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SEQUENCE
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Weiss J.B., Lote C.J., Bobinski H.;

Weiss J.B., Lote C.J., Bobinski H.;

Wew Lote C.J., Bobinski H.;

Wew Lote Wew Biol. 234:25-26(1971).

-!- FTM: S-LINKED GLYCAN CONSISTS OF GLC-GLC TRISACCHARIDE.

-!- PTM: S-LINKED GLYCAN CONSISTS OF THE GLYCOPROTEIN FROM WHICH THIS

PEPTIDE IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN

ATTRIBUTED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE.
MEDILINE-87005252; PubMed-3093276;
MEDILINE-87065252; PubMed-3093276;
MOLI M., Tanaka H., Sakagami Y., Isogai A., Fujino M., Kitada C.,
White B.A., An F.Y., Clewell D.B., Suzuki A.;
"Isolation and structure of the Streptococcus faecalis sex pheromone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CIA_ENTFA STANDARD; PRT; 7 AA.

P11932;
01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
01-OCT-1999 (Rel. 17, Last annotation update)
Sex pheromone CAM373 (Clumping-inducing agent) (CIA).
Bacteriococcus faecalis (Streptococcus faecalis)
Bacteria: Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCBL_TAXID=1351;
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                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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-! SIMILARITY: C-FERMINAL TO THE PHEROMONES CPD1 AND CAD1.
PIR; A25269; A25269.
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-!- FUNCTION: CAM373 INDUCES MATING RESPONSE OF DONOR CELLS
HARBORING PAM373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 14; DB 1; Length 10;
Pred. No. 4.5e+03;
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239BFEEAA1F5B1E8 CRC64;
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28.0%; Scor.
100.0%; Pred. No.
0; Mismatches
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                                                                                       Erythrocyte membrane glycopeptide
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50.0%;
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Matches 2; Conservative
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                                                                                                                 Homo sapiens (Human)
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nes 2; Conserv
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093135 acinetobact 091ww2 schizophyll 025355 locusta mig 09x884 equus cabal 095m70 trichosurus 090x78 psittacus e 090x88 prittacus e

008979 mus musculu Q47561 escherichia Q60192 spiroplasma

Ogumc7 homo sapien 034909 locusta mig 089457 petrolishe 08332 murine hepa 98322 streptomyce 090493 homo sapien 050194 spiroplasma 055837 rhizobium l 055837 rhizobium l 055837 rhizobium l 055837 chizobium l 055837 chizobium l 055837 chizobium l 095916 pinus taeda 09456 pinus taeda 09456 pinus taeda 094916 qiycine max 09936 beta vulgar 099918 petrius sp. 097505 escherichia

29agp4 arthrobacte

Perfect score:

Title:

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Scoring table:

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Database

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P82445.

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ID P82445.

ID 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)

DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)

DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana. NCBL_TaxID=4097;
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           047561
066192
093135
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097847
093480
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Q47505
O99182
Q9AGP4
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-!- TISSUE SPECIFICITY: XYLEM.
  008979
 Query Match
Best Local Similarity 42.9
Matches 3; Conservative
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  Planta 0:0-0(2000)
Cell wall.
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 Q938P2 beaudomonas
P83066 bacillus ce
Q96q19 homo sapien
Q95x03 hepatitis b
Q9xx08 boophilus m
P83161 anabaena sp
Q95nb1 eulemur ful
Q95nb0 eulemur ful
Q95nb0 eulemur ful
Q95nb0 eulemur ful
Q95nb0 excharomyc
Q47410 escherichia
Q9748 drosophila
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                                                                  December 19, 2002, 16:48:49; Search time 37 Seconds (without alignments) 55.688 Million cell updates/sec
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      GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Listing first 45 summaries
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Q14277
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PRELIMINARY;

014277

RESULT 2 Q14277 ID Q142

P92762 Q05403 Q47410 Q9H4M8 Q9VV82

Score

Result Š. 2

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AA09625.1; -.
927 MW; 69D6D7273B5726F0 CRC64;
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                                                             34.0%;
75.0%;
EMBL; AJ011482; CAA09625.1;
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Best Local Similarity 50.uv
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                        7 AA;
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3 GVLFLL 8
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Izeta A., Smerdou C., Alonso S., Penzes Z., Mendez A., Plana-Duran J.,
Enjuanes L.;
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-9436753; PubMed=8084609;
CECCHETINI I., Hofstra R., Yin L., Stulp R., Barone V., Stelwagen T.,
Bocciardi R., Nijveen H., Bolino A., Seri M., Ronchetto P., Pasini B.,
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MEDLINE=95159435; PubMed=7856095;
Elecute J., Rasschaert D., Lambert P., Levy L., Vende P., Laude H.;
"Complete sequence (20 kilobases) of the polyprotein-encoding gene 1 of transmissible gastroenteritie virus.";
virology 206:817-822(1995).
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01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical fusion protein.
Hypothetical fusion protein.
Transmissible gastroenteritis virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.
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MEDLINE-88078100; Pubmed=2825819;
Rapschaert D., Gelfi J., Laude H.;
Enteric coronavirus TGEV: partial sequence of the genomic RNA its organization and expression.";
Biochimie 69:591-600(1987).
                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae, Homo.
                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=94071887; PubMed=7902707;
Ceccherini I., Bocciardi R., Luo Y., Pasini B., Hofstra R.,
Takahashi M., Romeo G.;
"Exon structure and flanking intronic sequences of the human RET
proto-oncogene.";
Biochem. Biophys. Res. Commun. 196:1288-1295(1993).
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Pred. No. 6.7e+05;
1: Mismatches 2; Indels
                                       01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NOV-1998 (TrEMBLrel. 08, Last annotation update) RET protein short form (Fragment).
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                          01-NOV-1996 (TrEMBLrel. 01, Created)
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50.0%;
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                                                                                                           Homo sapiens (Human).
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Best Local Similarity
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1 RISHAF 6
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Submitted (JUL-2001) to the SWISS-PROT data bank.
-!- CATALYTIC ACTIVITY: ATP + D-FRUCTOSE 6-PHOSPHATE = ADP + D-
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NCBI_TaxID=1396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Quaternary ammonium compound-resistance protein QacEdeltal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2001 (TrEMBLrel. 13, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
6-phosphofructckinase (EC 2.7.1.11) (Phosphofructckinase)
(Phosphohexokinase) (Fragment).
Score 17; DB 12; Length 7; Pred. No. 6.7e+05; 1; Mismatches 0; Indels
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--- PATHWAY: KEY CONTROL STEP OF GLYCOLYSIS.

--- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

--- INDUCTION: BY SALT STRESS.

--- SIMILARITY: BELONGS TO THE PHOSPHOFRUCTOKINASE FAMI
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STRAIN=N;
MEDLINE=99297341; Pubmed=10368952;
Campbell N.J.H., Barker S.C.;
Campbell N.J.H., Barker S.C.;
Withe novel mitochondrial gene arrangement of the cattle tick,
Boophilus microplus: fivefold tandem repetition of a coding region.";
Mol. Biol. Evol. 16732-740(1999).
EMBL; AFI10616; AAD28386.1; -.
NON_TER
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                                                                                                                                                                                                                                      Boophilus microplus (Cattle tick).
Mitochondrion.
Bukaryota; Matazoa; Arthropoda; Chelicerata; Arachnida; Acari;
Parasitiformes; Ixodida; Ixodidae; Boophilus.
NCBI_TaxID=6941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P83161,

OLDEC-2001 (TEMBLEEL. 19, Created)

01-DEC-2001 (TEMBLEEL. 19, Last sequence update)

01-JUN-2002 (TEMBLEEL. 21, Last annotation update)

Putative RNA-binding protein rbpA (Fragment).

Anabaena sp. (strain L31).

Bacteria; Cyandbacteria; Nostocales; Nostocaceae; Anabaena.
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                                                                                                                                                          01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
ATP synthase 6 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER 1 1 SEQUENCE 8 AA; 938 MW; 58BB14404B5735B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Apte S.K., Uhlemann E., Schmid R., Altendorf K., Submitted (OCT-2001) to the SWISS-PROT data bank.-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
InterPro; IPR000504; RNA_rec_mot.
PROSTIE; PS00030; RRM_RNP_L; PARTIAL.
RNA-binding.
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                    2 VRIGHLYIL 10
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1 MQLFHLXLI 9
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EMBL; AB661211; BA854961.1; -. Ribosomal protein.

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NON_TER 10 10
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MEDILINE-21429115; pubmed-11543634;
Kenmochi N., Suzuki T., Uechi T., Magoori M., Kuniba M., Higa S.,
Watanabe K., Tanaka T.;
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MEDLINE-92013147; PubMed=1717588;
MEDLINE-92013147; PubMed=1717588;
Takahashi K., Kishimoto S., Ohori K., Yoshizawa H., Machida A., Ohuuma H., Tsuda F., Munekata E., Miyakawa Y., Mayumi M.;
"Molecular heterogeneity of e antigen polypeptides in sera from carriers of hepatitis B virus.";
J. Immunol. 147:3156-3160(1991).

NON_TER 10 10
SEQUENCE 10 AA; 1238 MW; 485A6E3AE72IE9C7 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
E antigen P20E (Fragment).
Hepatitis B virus.
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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                                                Score 16; DB 2; Length 10;
Pred. No. 1.2e+04;
0; Mismatches 1; Indels
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Pred. No. 1.2e+04;
3; Mismatches 0; Indels
NON_TER 10 10 SEQUENCE 10 AA; 1061 MW; 6A9D98A732C87044 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Mitochondrial ribosomal protein S30 (Fragment).
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                                             Query Match 32.0%;
Best Local Similarity 80.0%;
Matches 4; Conservative
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Local Similarity 25.0%;
les 1; Conservative
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7 HIFV 10
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RA MEDLINE-97153820; PubMed=9000751;

RA MEDLINE-97153820; PubMed=9000751;

RA MEDLINE-97153820; PubMed=9000751;

RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;

RT Replication slippage may cause parallel evolution in the secondary structures of mitochondrial transfer RNAs.";

RL Mol. Biol. Evol. 14:30-39(1997).

DR EMBI: U71325; AAC62249.1;

DR EMBI: U71325; AAC62249.1;

FT MON_TER 10 10

SEQUENCE 10 AA; 1246 MW; DBD38E27336401ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zumstein E., Pearson B.M., Kalogeropoulos A., Schweizer M.;
"A 29.425 kb segment on the left arm of yeast chromosome XV contains more than twice as many unknown as known open reading frames.";
Yeast 11:975-986(1995).
EMBL: X83121; CAA58183.1; -..
SGD; SO005456; COG3.
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Iguania, Acrodonta, Agamidae, Uromastycinae,
                                                                                                                     MEDLINE=97153826; PubMed=9000757; Macey J.R., Larson A., Ananjeva N.B., Fang Z., Papenfuss T.J.; Macey J.R., Larson A., Ananjeva N.B., Fang Z., Papenfuss T.J.; Two novel gene orders and the role of light-strand replication in rearrangement of the vertebrate mitochondrial genome."; Mol. Biol. Evol. 14:91-104(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBL_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER 8 AA; 879 MW; 7B5322D2C441E058 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA for ORF'S from chromosome XV (Fragment).
COQ3 AND YOL096C.
Saccharomyces cerevisiae (Baker's yeast).
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STRAIN=FY1679;
MEDLINE=96021609; PubMed=8533473;
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ilarity 28.6%;
Conservative
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Uromastyx acanthinura.
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Matches 2; Conserv
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SEQUENCE FROM N.A.
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2 MAHRWLL 8
                Mitochondrion.
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Wyner Y.M., Johnson S.E., Desalle R.;
Wyner Y.M., Johnson S.E., Desalle R.;
Wyner A.M., Johnson S.E., Desalle R.;
Submitted assessment of a red-fronted/white-collared lemur hybrid
zone at Andringitra,
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF258177; AAK53157.1; -.
NON_TER
1 1 1
NON_TER 10 10
SEQUENCE 10 AA: 1020 MW; DD492E6AFAF2C9D2 CRC64;
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SPOUROR FROM N.A.
Whyer Y.M., Johnson S.E., DeSalle R.;
Whyer Y.M., Johnson tof a red-fronted/white-collared lemur hybrid zone at Andringitra, Madagascar.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF258167; AAK53147.1; -...
NON_TER
                                                                                                           Malic enzyme (Fragment).
Bulemur fulvus (brown lemur).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Strepsirhini; Lemuridae; Eulemur.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Malic enzyme (Fragment).
Bulemur fulvus (brown lemur).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Strepsirhini; Lemuridae; Bulemur.
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Pred. No. 1.9e+04;
3; Mismatches 0; Indels
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Pred. No. 1.9e+04;
3; Mismatches 0; Indels
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01,MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Cytochrome c oxidase subunit I (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                             01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                               10 AA.
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                                                              -DEC-2001 (TrEMBLrel. 19, Created)
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25.0%;
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MEDLINE-85160860; PubMed=2580099;
WGDLINE-85160860; PubMed=2580099;
WGDLINE-85160860; PubMed=2580099;
WGDLINE-85160860; PubMed=2580099;
WGDLINE-8516080; Capalication control region of the IncFII R-plasmid NRI in vitro and in vivo.";
J. Mol. Biol. 188:395-410(1985).
Plasmid. X02302; CAA26166.1; -
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TISSUB-PERPHERAL BLOOD;
Pentecost B.T., Ling G.;
Pentecost B.T., Ling G.;
"The human pregnane X receptor promoter complex provides
transcriptional starts for a number of PXR related transcripts.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AY007189; AAG23345.1;
NON_TER
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=966;
                                                                                                                                                            Plasmid NR1.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
NCBL_TaxID=562;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Pot. repAX peptide (Fragment).
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 9 AA; 1055 MW; DCFA6412CDD1E87D CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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Matches 3; Conservative
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Search completed: December 19, 2002, 16:51:41 Job time : 59 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

December 19, 2002, 16:55:35; Search time 15 Seconds (without alignments) 51.272 Million cell updates/sec Run on:

US-09-692-401-6 42 Title: Perfect score:

1 RIGHLYIL 8 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

604 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 8

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	nt	on-monoxid	growth-modulating	sarcosine dehydrod	collagen alpha 1(ī	hypothalamic hepta	gramicidin S synth	Set	penalbumin - Adeli	T-cell receptor be	fatty-acid synthas	membrane protein -	sex pheromone cAM3	hypothetical L2 pr	gamma subunit of P	N-formyl oligopept	serum albumin - do	telomeric and tetr	angiotensin-conver	phytosulfokine alp	glutathione transf	hypothetical prote		aspartate transami	serine/threonine-s	tubulin beta-3 cha	cardioacceleratory	Ig H chain V-D-J r	phosphatidylethano
SUMMARIES	DI		PL0140	GKHU	A61419	B56979	NYPG7	S42407	A28709	A61467	PT0721	A60139	PQ0663	A25269	I56695	A48360	A60986	B45800	PC4373	PQ0009	JT0870	S71867	S08606	S45311	A11483	S58797	533567	S66646	PH1618	PN0043
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	Score	17	15	14	14	14	14	14	14	14	13	13	13	13	13	12	12	12	12	11	11	11	11	11	11	11	11	11	11	11
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Gaps

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Query Match 35.7%; Score 15; DB 2; Length 4; Best Local Similarity 66.7%; Pred. No. 2.8e+05; Matches 2; Conservative 1; Mismatches 0; Indels

2 IGH 4 :|| 1 MGH 3

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telomeric and tetr cytochrome oxidase R-phycoerythrin ga hypothelical prote Y protein - human T-cell receptor be neuropeptide GNFFR glutathione transf amine oxidase (cop NADH2 dehydrogenas anglotensin-conver acylase - Kluyvera Ig gamma chain C Igfactory receptor T-cell receptor T-cell receptor	LIGNMENTS  LIGNMENTS  erina mitochondrion serina n 03-Feb-1994 #text_change 07-Dec-1999 , K.L. 24.5 kilobase pair cytochrome oxidase subunit 4722; PMID:2558809 4722; PMID:2558809  ering the series of the series o	1) large chain - Pseudomonas carboxydohydroy'-Sep-1990 #text_change 28-Apr-1993 Meyer, O. dehydrogenase structural genes in carboxydo.  ; PMID:2818128 consists of three polypeptide chains: large,
PC4372 T13818 F22565 S53595 I37263 PT0662 A718129 A71870 A318081 A319512 A319512 A319512 A319512 A319512 A319512 A319512 A319512 A319512 A319512	ALI anser anse sion 111y, 111y, 301247	genase (EC 1.2.99.2) carboxydohydrogena quence_revision 07-5s 35-341, 1989 istribution of CO del 138; MuID:90055678; in
	ora Sora Cori Cori Cori Cori Cori Cori Cori Cori	(EC doby reviews 198 tion ID:9
\$\$\$\$\$\$\$\$\$\document{\alpha}\$\do	- Podospora on Podospora equence_rev equence_rev MCD 06, 15,9 MCD 06, 18327; MUID: 8327; MUID: 8327; MUID: 10n	boxyconce_n boxyconce_n mce_n 341, ribut ribut ; MU
30 31 32 32 32 34 34 35 36 37 37 37 38 39 40 40 40 40 40 40 40 40 40 40 40 40 40	RESULT 1 18888 COI intron 16 protein - Podospora anse C): Species: mitochondrion Podospora anse C; Species: 03-Feb-1994 #sequence_revision C; Accession: 13888 #sequence_revision D; Mritle: DNA sequence analysis of the A; Recence number: A48327; MUID:90124 A; Accession: 13888 A; Accession: 13888 A; Accession: 13888 A; Accession: 13888 A; Status: preliminary A; Moiss references: GB:X55026; GB:M309 A; Genetic code: GGC3 C; Keywords: mitochondrion A; Genetic code: SGC3 C; Keywords: mitochondrion A; Genetic code: SGC3 C; Keywords: mitochondrion A; Genetic code: SGC3 C; Moiss references: GB:X55026; GB:M309 C; Keywords: mitochondrion A; Genetic code: SGC3 C; Moiss references: Matches 2; Conservative 2; Matches 2; Conservative 2; Matches 1: OLGH 4	SULT 2  10140  Thom monoxide dehydro  Species: Pseudomonas  Date: 07-Sep-1990 #se  Accession: PL0140  Thile: Monology and d  Thile: Homology and d  Reference number: PL0140  Molecule type: protei  Mosidues: 1-4 <kra>  Comment: Carbon-monox  Keywords: Oxidoreduct  Keywords: Oxidoreduct</kra>

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Cispecies: Bacillus brevis
Cispecies: Alo. 1944 1940
FRISTEIN: T.; Vater, J.; Kruft, V.; Wittmann-Liebold, B.; Franke, P.; Panico, M.; Mc D
FRBS Lett. 340, 3944, 1994
A;Tilla: Detection of 4-phosphopantetheine at the thioester binding site for L-valin
A;Reference number: $42407; MUID:94164305; PMID:8119405
A;Molecule type: protein
A;Residues: 1-7 <STE>
                                                                                                                                                                                                                                                                                                     Mypothalamic heptapeptide - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Accession: A01417
R;Chang, R.C.C.; Hungy, W.Y.; Arimura, A.; Redding, T.W.; Coy, D.H.; Saffran, M.; Kon Horm, Metab. Res. 13, 228-232, 1981
A;Title: Isolation, structure and synthesis of a heptapeptide with in vitro ACTH-rele A;Reference number: A01417; MUD:81213980; PMID:6263778
A;Accession: A01417
A;Molecule type: protein
A;Residues: 17 <CRA.
C;Superfamily: hypothalamic heptapeptide
C;Superfamily: hypothalamus
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C;Species: Bacillus cereus
C;Add:1988 #sequence_revision 22-Aug-1988 #text_change 30-Sep-1993
C;Accession: A28709
C;Accession: A28709
D:D; Hepburn, T. W.; Moos, M.; Mariano, P.S.; Dunaway-Mariano, D.
Biochemistry 27, 2229-2234, 1988
A;Title: Investigation of the Bacillus cereus phosphonoacetaldehyde hydrolase. Eviden
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Pred. No. 2.8e+05;
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A;Accession: A28709
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <0LS>
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60.0%;
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Matches 2; Conservative
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Best Local Similarity 60.0
Matches 3; Conservative
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B5679
B5679
B5679
B5679
Collagen alpha 1(II) chain - bovine (fragment)
N.Alternate names: collagen alpha 3(XI) chain
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 03-Oct-1995
C;Accession: B56979
E;Wu, J.J.; Eyre, D.R.
J. Biol. Chem. 270, 18865-18870, 1995
A;Title: Structural analysis of cross-linking domains in cartilage type XI collagen. Ins
A;Reference number: A56978; MuID:95370194; PMID:7642541
A;Reference number: B56979
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-6 < Wux>
A;Note: the residue designated "X" is modified Lysine in collagen 1(II) some cross-linke
                                                                                                                                                               growth-modulating peptide - human growth-modulating peptide - human growth-modulating peptide - human c; Species: Homo saptens (man)
C; Date: 15-Jun.2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C; Accession: A01421
R; Schlesinger. D.H; Pickart, L.; Thaler, M.M.
Experientia 33, 324-325, 1977
A; Title: Growth-modulating serum tripeptide is glycyl-histidyl-lysine.
A; Reference number: A01421; MUID:77162369; PMID:858356
A; Rocession: A01421
A; Molecule type: protein
A; Rocession: A01421
A; Mocession: A01421
A; Mocession: A01421
A; Molecule type: protein
A; Rocession: A01421
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membrane protein - porcine epidemic diarrhea virus (isolate Belgian CV777) (fragment)
C;Species: porcine epidemic diarrhea virus
B;Bridgen, A.; Duarte, M.; Tobler, K.; Laude, H.; Ackermann, M.
J. Gen. Virol. 14, 1795-1804, 1993
J. Gen. Virol. 14, 1795-1804, 1993
A;Reference number: J02191; MUID:93389433; PMID:8397280
A;Recession: PQ0663
A;Accession: PQ0663
A;Accession:
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N.Alternate names: clumping-inducing agent (CIA)
C;Species: Enterococcus faecalis
C;Decies: Bnar-1988 #sequence_revision 31-Mar-1988 #text_change 18-Jun-1993
C;Accession: A22269
R;Mori, M.; Tanaka, H.; Sakagami, Y.; Isogai, A.; Fujino, M.; Kitada, C.; White, B.A FEBS Lett. 206, 69-72, 1986
A;File: Isolation and structure of the Streptococcus faecalis sex pheromone, cAM373
A;Reference number: A25269; MUID:87005252; PMID:3093276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156695

hypothetical L2 protein (mistranslated) - human papillomavirus type 16 (fragment)

c)Species: human papillomavirus type 16

c)Species: human papillomavirus type 16

c)Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000

c)Accession: 156695

J. Virol. 61, 3295-3298, 1987

A)Title: Integration of human papillomavirus type 16 DNA sequences: a possible early A)Reference number: 156695; MUID:87311896; PMID:3041049

A)Accession: 156695

A)Status: translated from GB/EMBL/DDBJ
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Pred. No. 2.8e+05;
2; Mismatches 1; Indels
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                                                Length 7;
                                           Score 13; DB 2; I
Pred. No. 2.8e+05;
1; Mismatches 1;
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3 GYSY 6
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Matches
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A60139
fatty-acid synthase (EC 2.3.1.85) - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-May-2000
C;Accession: A60139
R;Hardie, D.G.; Dewart, K.B.; Aitken, A.; McCarthy, A.D.
B;Ochim. Biophys. Acta 828, 380-382, 1985
A;Title: Amino acid sequence around the reactive scrine residue of the thioesterase dome A;Recreace number: A60139; MUID:85175165; PMID:3921056
A;Accession: A60139
A;Molecule type: protein
A;Recreace number: A60139
A;Molecule type: protein
A;Recreace number: A60139
A;Molecule type: protein
C;Superfamily: rat fatty-acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase I home C;Superfamily: rat fatty-acid synthase; 3-oxoacyl-[acyl-carrier-protein] Syrtolase homology; short-chain alcohol dehydrogenase homology; multifunctional enz C;Keywords: acyltransferase; carrier protein; coenzyme A; homodimer; multifunctional enz F;5/Active site: Ser (of olecyl-carrier-protein] hydrolase) #status experimental
                                                                                                                                                                                                       RESULT 9
#61467
penalbumin - Adelie penguin (fragment)
C:Species: Pygoscelis adelie (Adelie penguin)
C:Species: Pygoscelis adelie (Adelie penguin)
C:Date: O7-Oct-1994 #sequence_revision 04-Nov-1994 #text_change 04-Nov-1994
C;Accession: A61467
R;Osuga, D.T.; Aminlari, M.; Ho, C.Y.K.; Allison, R.G.; Feeney, R.E.
R;Osuga, D.T.; Aminlari, M.; Ho, C.Y.K.; Allison, R.G.; Feeney, R.E.
A;Title: Sulfhydryl proteins of penguin egg white: ovalbumin and penalbumin. Comparisons
A;Reference number: A61467
A;Accession: A61467
A;Accession: A61467
A;Molecule type: protein
A;Residues: 1-8 <CSUP
C;Comment: Penalbumin is a major protein component of egg whites from penguins but not f
C;Keywords: egg white; glycoprotein
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Pr0721
T-cell receptor beta chain V-D-J region (140-2K) - mouse (fragment)
C. Species: Mus musculus (house mouse)
C. Species: Mus musculus (house mouse)
C. Date: 17-Unl-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C. Accession: PT0721
R. Feeney, A.J.
J. Exp. Med. 115-124, 1991
A. Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A. Reference number: PT0721
A. Fitle: Junctional sequences of hour in the profile of the profile and t
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Pred. No. 2.8e+05;
1; Mismatches 1;
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Best Local Similarity 50.0%;
Matches 2; Conservative
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2 KIDHV
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A; Molecule type: DNA
A; Residues: 1-7 <SCH>
A; Cross-references: GB:M30709; NID:g190253; PIDN:AAA65995.1; PID:g553616
C; Comment: This is the hypothetical translation of a viral sequence integrated into the C; Comment: It is translated in an incorrect, -1, reading frame of the L2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gramma subunit of Protein A - Methylosinus trichosporium (fragment)
C; Species: Methylosinus trichosporium
C; Species: Methylosinus trichosporium
C; Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C; Accession: A48360
R; Cardy, D.L.; Laidler, V.; Salmond, G.P.; Murrell, J.C.
Arch. Microbiol. 156, 477-483, 1991
A; Title: The methane monocygenase gene cluster of Methylosinus trichosporium: cloning A; Reference number: A48360; MUID:92153031; PMID:1785954
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-4 <CAR>
A;Cross-references: GB:S81887; NID:g245213; PIDN:AAB21391.1; PID:g245214
A;Note: sequence extracted from NCBI backbone (NCBIN:81887, NCBIP:81912)
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1 HSY 3
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litoria rub
litoria rub
pardachirus
mytilus edu
mytilus edu
                                                            sarcophaga
alcaligenes
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leptinotars
                                                                                                                                    mus musculu
                                                                                                                        litoria rub
                                                                                   haemonchus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- COFACTOR: Molybdenum (molybdopterin).
-!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                to carbon
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                            Kraut M., Hugendieck I., Herwig S., Meyer O.;
"Homology and distribution of CO dehydrogenase structural genes
carboxydotrophic bacteria.";
Arch. Microbiol. 152:335-341(1989).
-!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carb
                                                                                                                                                                                                                                                                                                                                            group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dioxide.
-!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
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0
P82099
P82100
P81864 I
P13733 6
P13733 6
P11473 7
P16101 2
P41874 E
P4298 J
P41874 E
P42065 1
P38641 I
                                                                                                                                                                                                                                                    Ol-FEB-1991 (Rel. 17, Created)
Ol-FEB-1991 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO dehydrogenase subunit L) (CO-DH L) (Fragment).
                                                                                                                                                                                                                                                                                                                            Pseudomonas carboxydohydrogena.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae
Bradyrhizobiu;
NCBI_TaxID=290;
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21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last annotation update)
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                                                                                                                                                                      ALIGNMENTS
                       PAP2_PARMA
CIP1_MYTED
CIP2_MYTED
TMOF_SARBU
CHOX_ALCSP
FAR3_HAECO
FAR3_PANRE
MNP1_LEPDE
 EIO3_LITRU
EIO4_LITRU
                                                                                                                       TY51_LITRU
UF03_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=90055678; PubMed=2818128;
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llarity 66.7%;
Conservative
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Oxidoreductase; Molybdenum.
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P01157;
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SEQUENCE
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SEQUENCE.
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                                                                               December 19, 2002, 16:52:44; Search time 10 Seconds (without alignments) 33.181 Million cell updates/sec
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P82158
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P43171
P81010
P01151
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           GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                   112892 seqs, 41476328 residues
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HY7_PIG
CIA_ENTFA
GFRP_MOUSE
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UNO6_PINPS
ALL6_CYDPO
TPIS_CANFA
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FARP_MONEX
FAR5_HIRME
ACI_THUAL
UF06_MOUSE
EOSI_HUMAN
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FYRI_ANTEL
BIOB_CITFR
PRCT_PERAM
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AL18_CARMA
CAD1_ENTFA
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FUSS_FUSSO
THYL_PIG
FAR4_HIRME
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E105_LITRU
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Maximum Match 100%
Listing first 45 summaries
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GRWM_HUMAN
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                                                           protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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42
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length: 8
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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50.0%;
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les 2; Conserv
                                      NCBI_TaxID=9823;
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2 IFIL 5
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P99025;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                    Schlesinger D.H., Pickart L., Thaler M.M.;

Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";

Experientia 33:324-325(1977).

-i- MISCELLANEOUS: THIS SERUM TRIPEPTIDE HAS BEEN FOUND TO STIMULATE
GROWTH OF SOME CELL TYPES AND TO INHIBIT OTHER TYPES IN VITRO.

SEQUENCE 3 AA; 340 MW; 6331E8100000000 CRC64;
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Panagrellus redivivus.
Sukaryota, metazoa, Nematoda, Chromadorea, Ascaridida, Ascaridoidea,
Ascarididae, Ascaris.
NCBI_TaxID=6253, 6233;
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                                                                                                                                                                   33.3%; Score 14; DB 1; Length 3; 100.0%; Pred. No. 1.1e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ascaris suum (Pig roundworm) (Ascaris lumbricoides), and
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SEQUENCE 7 AA; 992 MW; 69D4073B5B11E350 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
FMRRAmide-like neuropeptide AF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last annotation update)
Hypothalamic heptapeptide.
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MEDLINE=93324431; PubMed=8332542;
      MEDLINE=77162369; PubMed=858356;
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50.0%;
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Les 2; Conserv
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HEYL 5
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P01153;
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FAR2_ASCSU
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ID HY7,
AC P01,
DT 21,
DT 21,
DT 21,
OF HYPO
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01-OCT-1989 (Rel. 12, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
Sex pheromone CAM373 (Clumping-inducing agent) (CIA).
Enterococcus faecalis (Streptococcus faecalis).
Bacteria: Airmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NUBL_TAXID=1351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-97005252; PubMed=3093276; MedLine-97005252; PubMed=3093276; Mori M., Tanaka H., Sakagami Y., Isogai A., Fujino M., Kitada C., White B.A., An F.Y., Clewell D.B., Suzuki A.; Isolation and structure of the Streptococcus faecalis sex pheromone,
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
MEDLINE-81213980; PubMed-6263778;
MEDLINE-81213980; PubMed-6263778;
MEDLINE-81213980; PubMed-6263778;
MEDLINE-81213980; PubMed-6263778;
Saffran M., Kong A., Hamilton J.W., Cohn D.V., Schally A.V.;
"Isolation, structure and synthesis of a heptapeptide with in vitro ACTH-releasing activity from porcine hypothalamus.";
Horm. Metab. Res. 13:228-232(1981).
PIR; A01417; NYPG7.
SEQUENCE 7 AA; 957 MW; 632B45B1FB5059A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
GTP cyclohydrolase I feedback regulatory protein (P35) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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-! FUNCTION: CAM373 INDUCES MATING RESPONSE OF DONOR CELLS
- HARBORING PAM373.
-! MISCELLANEOUS: THE N-TERMINUS IS POSSIBLY RESPONSIBLE FOR SPECIFFCITY OF PHEROMONES TO PLASMIDS.
-! SIMILARITY: C-FERMINAL TO THE PHEROMONES CPD1 AND CAD1.
PIR: A25269; A25269.
                                                                                                                                                                                                                                                                                                                         33.3%; Score 14; DB 1; Length 7; 60.0%; Pred. No. 1.10+05; ive 0; Mismatches 2; Indels
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Pred. No. 1.1e+05;
2; Mismatches 0;
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Gaps

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16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Phytosulfokine-alpha (PSK-alpha) [Contains: Phytosulfokine-beta (PSK-beta)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEOUGNCE, AND IDENTIFICATION BY MASS SPECTROMETRY.

STRAIN=CV. US-Harumakigosun;

MEDLINE=20212743; PubMed-10750705;

Hanai H., Matsun T., Yamamoto M., Matsubayashi Y., Kobayashi T.,

Ramada H., Sakagami Y.,

Kamada H., Sakagami Y.,

Kamada H., Sakagami Y.,

Kamada H., Sakagami Y.,

A secreted peptide growth factor, phytosulfokine, acting as a
stimulatory factor of carrot somatic embryo formation.";

Plant Cell Physiol. 41:27-32(2000).

-!-FUNCTION: IN PRESENCE OF 2,4-D, STIMULATES PROLIFERATION OF THE
CELLS, BUT DOES NOT STIMULATE DIFFERENTIATION INTO THE SOMATIC

EMBRYOS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -:- SUBCELLULAR LOCATION: Secreted.
-:- PTM: SULFATION IS IMPORTANT FOR ACTIVITY AND FOR THE BINDING TO PUTATIVE MEMBRANE RECEPTOR (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO THE PHYTOSULFOKINE FAMILY.
Growth factor; Sulfation.
PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
NCBL_TaxID=4039;
                    Indels
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                                                                                                                                                                                                                                                                                                26.2%; Score 11; DB 1; Length 5; llarity 100.0%; Pred. No. 1.1e+05; Conservative 0; Mismatches 0; Indels
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(Rel. 38, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Daucus carota (Carrot).
                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 2; Conserv
  NCBI_TaxID=132421;
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P81675;
15-JUL-1999 (
15-JUL-1999 (
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MOD_RES
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2 YI 3
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P58261;
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UNO6_PINPS
ID UNO6_P:
AC P81675,
DT 15-JUL.
DT 15-JUL.
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PSK_DAUCA
PSK_DAUCA
AC P5826
DT 16-0C
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PA1873;
01-NOY-1995 (Rel. 32, Created)
01-NOY-1995 (Rel. 32, Last sequence update)
01-NOY-1995 (Rel. 32, Last annotation update)
NOY-1995 (Rel. 32, Last annotation update)
Artioposthia enuropeptide RYIRF-amide.
Artioposthia triangulata.
Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida; Terricola; Geoplanidae; Arthurdendyus.
                                                           Sanchez J.-C., Rouge V., Frutiger S., Hughes G., Yan J.X.,
Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,
Cowthorne M.; Appel R.D., Binz P.-A., Hochstrasser D.F.,
Submitted (AuG-1998) to the SWISS-PROT data bank.
-!- FUNCTION: MEDIATES TETRAHYDROBIOPTERIN INHIBITION OF GTP
CYCLOHYDROLASE I. THIS INHIBITION IS REVERSED BY L-PHENYLALANINE
(BY SIMILARITY).
-!- SUBMIT: HOMODIMER (BY SIMILARITY).
SWISS- 2DPAGE: P99025; MOUSE.
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Borgheres1 R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;

Borgheres1 R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;

Borgheres1 R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;

Borgheres1 R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;

Foodp. and Gentification of anglotensin-like peptides from the plasma of the snake Bothrops jararaca.";

Comp. Biochem. Physiol. 113B:467-473(1996).

InterPro. IPRO00215; Serpin.

PROSITE; PS00284; SERPIN; PARTIAL.

Versoconstrictor; Plasma; Serpin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Anglotensin-like peptide II (Fragment).
Bothrops Jararca (Jararca).
Eukaryota; Metazoa; (Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Coctallinae; Bothrops.
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Pred. No. 1.18+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;
                                                                                                                                                                                                                                                                                                                       7 AA; 806 MW; 71B5B057273B4700 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 AA.
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ilarity 66.7%;
Conservative
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66.7%;
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Best Local Similarity
Matches 2; Conserv
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                                              TISSUE-Liver;
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ID ANG2_BOTJA
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3 VYI
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TISSUE-Heart;

MEDLINE-98163340; PubMed-9504812;

Dunn M.J. Corbett J.M., Wheeler C.H.;

"HSC-2DPAGE and the two-dimensional gel electrophoresis database of dog heart proteins.";

Electrophoresis 18:2795-2802(1997).

-: CATALYTIC ACTIVITY: D-91yceraldehyde 3-phosphate = glycerone
                                                                                                                                                                                                                                                                                                                                                                                        -i- PATHWAY: PLAXS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.
-i- SUBULIT: HOMODINER (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
HSC-2DPAGE; P54714; DGG.
InterPro; IPR000652; Triophos_ismrse.
PROSITE; P500171; TIM, PARTIAL.
Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
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01-0c7-1994 (Rel. 30, Last sequence update)
01-0c7-1994 (Rel. 31, Last sequence update)
01-FBB-1995 (Rel. 31, Last annotation update)
Unknown protein from 2D-page of fibroblasts (P19) (Fragment).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                    Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Carnivora, Fissipedia; Canidae, Canis.
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Pred. No. 1.1e+05;
2; Mismatches 0; Indels
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Les 2; Conservative
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Best Local Similarity
1; Conserve
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                                                                                                        NCBI_TaxID=9615;
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2 VGN 4
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FARP_MONEX
ID FARP_MONEX
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P38639;
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Bukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Hexapoda,
Busecta, Petrygota, Neoptera, Endopterygota, Lepidoptera, Glossata,
Ditrysia, Tortricoidea, Tortricidae; Olethreutinae, Cydia.
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MEDLINE-99274088; PubMed=10344291;
Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
Frigerio J. M., Plomion C.;
"Separation and characterization of needle and xylem maritime pine
                                                                                                                                                                                                                                                                                                                                                           Electrophoresis 20:1098-1108(1999).
--- MISCELLANEOUS: ON THE 2D-GEL THE DEFERMINED PI OF THIS UNKNOWN PROTEIN IS: 6.6, ITS MW IS: 25 kDa.

NON_TER 1 1
                                                    Pinus pinaster (Maritime pine).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
NCBL_TaxID-71647;
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SEQUENCE:

TISSUE-Larva;

MEDLINE-98054539; PubMed-9392829;

Bove H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley i Duvey M., East P.D., Thorpe A.D. Thorpe T.D. Thorpe
15-JUL-1999 (Rel. 38, Last annotation update) (Fragment). Unknown protein from 2D-page of needles (N141) (Fragment).
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01-0cT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Fragment).
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100.0%; Pred. No. 1.1e+05;
tive 0; Mismatches 0;
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30-MAY_2000 (Rel. 39, Last sequence update)
30-MAY_2000 (Rel. 39, Last annotation update)
Cydiastatin 6.
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P54714;
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SEGUENCE.
MEDLINE-9312289; PubMed-8323531;
MAILE A.G., Shaw C., Halton D.W., Thim L.;
MAILE A.G., Shaw C., Halton D.W., Thim L.;
"GRFRFRAmide: a novel FMRPamide-immunoreactive peptide isolated from "GRFRFRAmide: a novel FMRPamide expansa"; Life sheep tapeworm, Moniezia expansa"; 1054-1060(1993).
Biochem. Biophys. Res. Commun. 193:1054-1060(1993).
-I. SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
FAMILY.

AMIDATION.

AMIDATION.
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
01-NOV-1995 (Rel. 32, Last annotation update)
FMREanide-like neuropeptide GGXYMRP-amide.
Hirudo medicinalis (Medicinal leech)
BUXATYOTA; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudinea
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        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
FMRFamide-like neuropeptide GNFFRF-amide.
Monlezia expansa (Sheep tapeworm).
Bukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
Cyclophyllidea; Anoplocephalidae; Moniezia.
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23.8%; Score 10; DB 1; Length 6;
Best Local Similarity 25.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 2; Mismatches 1; Indels
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SEQUENCE 7 AA; 858 MW; 69D4068B53387810 CRC64;
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ateles fusc
macaca mula
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talpa altai
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P82445 P82445 PRELIMINARY; PRT; 7 AA.
P82445.
01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
Noction and Labacum (Common tobacco).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; eussterids I; Solanales; Solanaceae; Nicotiana.
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STRAIN-CV. PETIT HAVANA;
STRAIN-CV. BODHAM V.A., Mitchell G.P., Robertson D., Slabas A.R.,
Blee K.A., Bonham U.A., Mitchell G.P.,
Wojtaszek P., Bolwell G.P.;
"Proteomic study of secondary cell wall proteins from transformed
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panta 0:04(200).
-! STUBCELLULAR LOCATION: CELL WALL.
-! TISSUE SPECIFICITY: XYLEM.
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093182 gratholebia
095871 canis famil
047505 escherichia
09r762 bochera ap
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09r762 escherichia
09r761 boch osapien
09uhk1 homo sapien
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O9yq10 transmissib
                                                                                       2002, 16:54:55; search time 42 Seconds (without alignments) 39.247 Million cell updates/sec
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Copyright (c) 1993 - 2002 Compugen Ltd.
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MEDLINE-99297341; PubMed=10368952; Campbell N.J.H., Barker S.C.; Campbell N.J.H., Barker S.C.; "The novel mitochondrial gene arrangement of the cattle tick, Boophilus microplus: fivefold tandem repetition of a coding region."; Mol. Biol. Evol. 16:732-740(1999).

Mitochondrion.
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Chave K.J., Sanders P.G.;

Chave K.J., Shall K., Sanders P.G.;

Chave List and characterisation of human genomic sequences encoding cytosolic serine hydroxymethyltransferase.";

Biochem. Soc. Trans. 25:53-53(1997).

EMBL; Y14492;

EMBL; RAB4441;

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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Buteleostomi;
Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Parasitiformes; Ixodida; Ixodidae; Boophilus.
NCBL_TaxID=6941;
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llarity 50.0%; Pred. No. 6.7e+05;
Conservative 1; Mismatches 1; Indels
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Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
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8 AA; 868 MW; 7C205721E44AB5B8 CRC64;
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8 AA; 938 MW; 58BB14404B5735B0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                  Boophilus microplus (Cattle tick).
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es 3; Conservative
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MEDLINE-99099045; PubMed-9882359;
Izete A., Smerdou C., Alonso S., Penzes Z., Mendez A., Plana-Duran J.,
Enjuanes L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-95156435; PubMed=7856095;
Eleouet J., Rasschaert D., Lambert P., Levy L., Vende P., Laude H.;
Elconette sequence (20 kilobases) of the polyprotein-encoding gene 1
of transmissible gastreenteritie virus.";
Virology 206:817-822(1995).
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MEDLINE-88078100; PubMed=2825819;
MEDLINE-88078100; PubMed=2825819;
MSSSCHEART D., Gelfi J., Laude H.;
Enseric coronavirus TGEV: partial sequence of the genomic RNA its organization and expression.";
Biochimie 69:591-600(1987).
EMBL; AJOI1482; CAGO(2521; -..
SEQUENCE 7 AA; 927 MW; 69D6D727385726F0 CRC64;
                       01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLRel. 19, Last annotation update)
Hypothetical fusion protein.
Transmissible gastroenteritis virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                      "Replication and packaging of transmissible gastroenteritis coronavirus-derived synthetic minigenomes."; J. Virol. 73:1535-1545(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Quaternary ammonium compound-resistance protein QacEdeltal
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STRAIN=YMO704; TRANSPOSON-CLASS I INTEGRON;
Lee K., Chong Y., Yum J.H., Yong D., Livermore D.M.;
"VIM-2 metallo-beta-lactamase gene-containing integron in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.5%; Score 17; DB 12; Length 7; 75.0%; Pred. No. 6.7e+05; Live 1; Mismatches 0; Indels
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AY029772; AAK50441.1; ...
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01-DEC-2001 (TrEMBLrel. 19, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last seno
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Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                                                                           NCBI_TaxID=11149;
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SEQUENCE FROM N.A.
MEDLINE-20022990; PubMed-10555290;
Clark M.A., Moran N.A., Baumann P.;
Sequence evolution in bacterial endosymbionts having extreme base compositions.";
Mol. Biol. Evol. 16:1586-1598(1999).
EMBL; AF130812; AAF13797.1; -.
SEQUENCE 8 AA; 980 MW; F3A73B504771A336 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                        Query Match 26.2%; Score 11; DB 2; Length 8; Best Local Similarity 33.3%; Pred. No. 6.7e+05; Matches 1; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Buchnera aphidicola.
Bacteria: Proteobacteria: gamma subdivision; Buchnera.
NCBI_TaxID=9;
                                                                                                                   Proteobacteria; gamma subdivision; Buchnera.
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2001 (TrEMBLrel. 17, Last annotation update)
Nifs protein homolog (Fragment).
NIFS.
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01-MAY-2000 (TrEMBirel. 13, Last sequence update)
01-MAY-2000 (TrEMBirel. 13, Last annotation update)
Nifs protein homolog (Fragment).
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                                                                                                 Buchnera aphidicola.
Bacteria; Proteobact
                                                                                                                                      NCBI_TaxID=9;
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Q9R7T2
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                                                                                                                                                                        SEQUENCE FROM N.A.

BEDILBELGY0432323 PubMed-88940533,
Wenta P.J., Broulllette J.A., Yuzbasiyan-Gurkan V., Brewer G.J.,
Wenta P.J., Broulllette J.A., Yuzbasiyan-Gurkan V., Brewer G.J.,
"Gene-specific universal mammalian sequence-tagged sites: application
to the canine genome."
Biochem. Genet. 34:321-341(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=96099297; Pubmed-8522520;
GONZAIS-PASSTON J.E., San Millan J.L., Castilla M.A., Moreno F.;
GONZAIS-PASSTON J.E., San Millan J.L., Castilla M.A., Moreno F.;
Structure and organization of plasmid genes required to produce the translation inhibitor microcin C7.";
J. Bacteriol. 177:7131-7140[1995).
EMBL, X5583; CA440808.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Venta P.J., Cao Y., Alexander L., Yuzbasiyan-Gurkan V.;

"Dinucleotide repeat polymorphism in the canine retinoblastoma (RB1) gene.";

Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

EMBL: AF155737, AAD38807.1; -.

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                                                                       nosis familiaris (Dog).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBL_TaxID-9615;
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asteria: Froteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 19, Last annotation update)
01-DRC-2001 (TrEMBLRel. 19, Last annotation update)
01-NOV-1999 (TrEWBLrel. 12, Last sequence update) 01-NOV-1999 (TrEWBLrel. 12, Last annotation update) Retinoblastoma protein (Fragment).
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SEQUENCE 8 AA; 895 MW; 1425BB18676721E3 CRC64;
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Ambrose H.J., Chambers S., Mieli-Vergani G., Robertson N.H.,
Newton C.R., Ferrie R.M.;
Wolecular characterisation of a new alpha-1-antitrypsin M variant
allele, Mynitstable: implications for DNA-based diagnosis.";
Diagn. MOJ. Pathol. (0.0012000).
EMBL; AF159454; AAF15128.1;
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SEQUENCE 8 AA, 838 MW; 84A732CDD331F2CD CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Alpha-1-antitrypsin M-variant (Fragment).
Alm.
Alm.
Bomo sapiens (Human).
Bukaryota, Wetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Local Similarity 40.0%: Fred. No. 6.7e+05; Indels
Local Similarity 40.0%: Fred. No. 6.7e+05; Indels
Local St. Conservative 1; Mismatches 2; Indels
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                       SEQUENCE FROM N.A.
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CDB; cytotoxic T lymphocyte; cancer; carcinoma; melanoma; myeloma;
brain tumour; sarcoma; vaccine; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antigenic peptides derived from MAGE-Al2 polypeptides, useful diagnosis and treatment of cancer, such as bladder, lung, breast,
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  19-OCT-2000; 2000WO-US28852
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WO200129220-A2.
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 MAGE-A12 human leu
MAGE2 HLA-B7 super
Tumour associated
MAGE2 derived HLA
Peptide obtained b
Substrate #1 for c
Angiotensin I conv
AGE derived peptid
Peptide determined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                      (without alignments)
31.353 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                Description
                                                                          December 19, 2002, 16:52:04; Search time 34 Seconds
          GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                  908470 segs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE02084
AAG84724
AAB76090
ABJ00185
AAW79124
AAW17691
AAW87243
AAW87243
                                                     protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length
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1 RIGHLYIL 8
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64.3
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are present invention describes makely epilopes (1), also described are present invention describes makely epilopes (1); also described and binds to a complex of (1); (2) a peptide (TI) comprising (I) and a second epitope and has less than 50 contiguous amino acids; (3) a vaccine composition comprising (II), a unit dose of a peptide with at least 50 configuous amino acids with 100% identity to the nature peptide sequence of MAGE2/3, and a pharmaceutical excipient; (4) an isolated nucleic acid encoding (I); and (5) an isolated nucleic acid encoding (II). (1) has crytostatic activity, and can be used in vaccines and as an immunostimulant. A vaccine of (3) is useful for monitoring or evaluating and prevention of cancer. (I) is useful for monitoring or evaluating and prevention of cancer. (I) is useful for monitoring or evaluating and prevention of cancer. (I) is useful for monitoring or evaluating and patient with (I) that binds to a human leukocyte antigen (HLA) allele present in the patient and detecting the presence of the T-lymphocyte that binds to the peptide. The vaccine allows the opportunity to combine epitopes derived from multiple tumour associated molecules reducing the likelihood of frumour secape due to antigen loss. AAGM$15 to AAGM$4999 and AAB99725 represent amino acid sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human leukocyte antigen; HLA; major histocompatibility complex; MHC; yctocoxic T lymphocyte; CTL; human class I MFC; immunogenic; HLA binding peptide; fumune response; glycoprotein; cytostatic; virucide; hepatotropic; antiinflammatory; anti-HIV; vaccine; chamman immunodeficancy virus; protococide; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; human papilloma virus; HPV; cytomegalovirus; CMV; acquired immunodeficiency syndrome; AIDS; renal carcinoma; cervical carcinoma; lymphoma; malaria; cordiance accordiance acuminatum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
    present invention describes MAGE2/3 epitopes (I). Also described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Composition comprising human leukocyte antigen binding peptide which comprises isolated, prepared epitope useful for treating viral infections such as acquired immunodeficiency syndrome, and cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            64.3%; Score 27; DB 22; Length 8; 83.3%; Pred. No. 7.8e+05; 1ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumour associated antigen MAGE2 immunogenic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB76090 standard; Peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sette A, Sidney J, Southwood S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 47; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JUN-2000; 2000WO-US17842.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 83.3
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                                                                                                                                                                                                                                                                                                                                                                                 present invention
                                                                                                                                                                                                                                                                                                                                                                                                                          8 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QQ
  The patent discloses antigenic peptides derived from MAGE-A12

protein and presented by human leukocyte antigens (HLAS). These
antigenic peptides when presented by an antigen presenting cell
having a HLA class I molecule, effectively induce the activation
and proliferation of COBH eyrotoxic T lymphocytes. MAGE-A12 is
useful for treating a subject having a disorder characterised by
comprision of MAGE-A12. The protein microarray comprising MAGE-A12

is useful for diagnosing a disorder, especially cancer, by determining
the binding of an antibody. T lymphocytes or a HLA molecule isolated
compression of MAGE-A12. MAGE-A12 is useful for treating cancers.

CC from the subject suspected of having the disorder characterised by the
expression of MAGE-A12 is useful for treating cancers.

CC colrectal carcinomas, melanomas, oesophageal, lung, head and
complete and renal carcinomas and to produce antibodies. MAGE-A12

contibodies are useful for diagnosing disorders characterised by
contibodies are useful for diagnosing disorders characterised by
antibodies are useful for diagnosing disorders characterised by
controlled and vaccines. They are also used in gene therapy.

CC MHC) and is recognised by CTLS.

(MHC) and is recognised by CTLS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; human leukocyte antigen; HLA epitope; cytotoxic T lymphocyte; CTL; MAGE2; MAGE3; melanoma antigen gene; immune response; vaccine; cancer; cytostatic; immunostimulant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            An isolated prepared MAGE2/3 epitope (I) for use in pharmaceuticals the treatment and prevention of cancer \dot{\,}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 42; DB 22; 100.0%; Pred. No. 7.8e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
brain, prostate and renal carcinomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 155; 171pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAG84724 standard; Peptide; 8 AA
                                           Claim 1; Page 43; 69pp; English.
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Best Local Similarity 100..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RIGHLYIL 8
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Synthetic.
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Keogh E;
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97WO-IB01508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Epstein-barr virus.
                                                                                                                             Query Match
Best Local Similarity
Matches 5; Conserv
                                                                              8 AA;
                                                                                                                                                                                                                   2 IGHLYI 7
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3 ISHLYI 8
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15-NOV-1996;
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                                                                                    Sequence
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The present invention describes a composition (1) which comprises at least one human leukocyte antigen (HLA) binding peptide comprising an isolated, prepared epitope comprising one of 547 8-11 residue amino acid sequences (51), given in AAB75803 to AAB76349. (1) has cytostatic, virucide, hepatotropic, antinflammatory, anti-HV (human immunodefichency virus) and protozocatide activities, which can be used in vaccine production and is an inducer of cytotoxic T-cell response. (1) is useful for inducing a cytotoxic T cell response against a preselected antigen in a patient expressing a specific major preselected antigen in a patient expressing a specific major of relative complexibility complex (MHC) class I allele, by contacting cytotoxic T cells (CTLs) from the patient with (1). (1) is useful as a vaccine to treat and/or prevent viral infection and cancer such as prostate cancer. Cytomegalovirus (CMV), acquired immunodeficiency syndrome (AIDS), renal carcinoma, cervical carcinoma, lymphoma, malaria, and condyloma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to compositions containing immunogenic peptides, which composites a B7-like-supermotif. The compositions can be used, as vaccines, to treat or prevent viral diseases (hepatitis B or C. Epstein-Barr, human immune deficiency, Lassa fever or cytomegaloviruses), cancers (e.g. of prostate, kidney or cervix, or lymphoma, where associated with expression of p53, carcino-embryonal antigen or Her2/neu), or malaria. The peptides are also useful as diagnostic agents, e.g. to predict the outcome of a particular therapy and to identify subjects at risk of developing a chronic infection. Nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New immunogenic peptide with B7-like supermotif, useful in vaccines against e.g. viral infection and cancer, induces a cytotoxic T cell response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human major histocompatability complex; HLA; immunogen; cancer; viral infection; vaccine; antigen; anti-HIV; virucide; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 8;
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Pred. No. 7.8e+05;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                64.3%;
83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 83.3
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8 AA;
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                                                                                                                                                                                                                                                                                                                                                              acuminatum.
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Sequences shown in AAW79110 to AAW79125 are obtained by oligomerisation of a selected minimal moutif by complementary oligonuclectides. The invention provides a method for increasing the resistance of a core protein to proteolytic degradation that comprises linking or inserting conto or into the core protein a stabilising polypeptide of formula of formula (Glya)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(Glyb)X(
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encoding the peptides can be used in DNA vaccines. The present sequence is an immunogenic peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fusion protein; stabilising polypeptide; proteolytic degradation; resistance; half-life; autoimmune disease; inflammation; nitro drug; Ikappa regulator protein; inflammatory bowel disease; in vivo imaging; nitroreductase protein; enzyme therapy; prodrug therapy; protease; cancer; pathological condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New fusion proteins resistant to proteolytic degradation - comprising a core protein with a stabilising polypeptide comprising a peptide sequence containing glycine repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                     Length 8;
                                                                                                                                                                                                                                                                                                     Score 27; DB 23; Length 8;
Pred. No. 7.8e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide obtained by oligomerisation of a minimal motif.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW79124 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                            64.3%;
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This invention relates to the preparation of angiotensin I converting enzyme (ACE) inhibitors by a microbiological process. The inhibitors are useful as hypotensive agents, and heat resistant ACE inhibitors are used in food processing. The invention includes examples of ACE I inhibitory peptides, represented by sequences AAB26858-B26868.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Angiotensin I converting enzyme; ACE; ACE inhibitor; hypotensive agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide production; fusion peptide; histidine tag; enterokinase; ACE
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anglotensin I converting enzyme inhibitory octapeptides useful as hyopensive agents, and a process for their preparation .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Angiotensin I converting enzyme (ACE) inhibitory peptide 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 24; DB 21; Length 8; Pred. No. 7.8e+05; Mismatches 1; Indels
                     Score 24; DB 18; Length 7; Pred. No. 7.8e+05; 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                          AAB26860 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU98271 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5; Page 2; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
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                     57.1%;
50.0%;
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                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                     Query Match
Best Local Similarity 50.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 50.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACE derived peptide P2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TOHA-) TOYO HAKKO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-614869/59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JP2000229996-A.
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                                                                                                              GHLYIL 8
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2 GHFFVL 7
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Glycine max.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                    30-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU98271;
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Matches
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                                                                                                                                                                                                                                   RESULT 7
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                                                                                                                                                           Dp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM17687-W17698 represent synthetic substrates for proteases known to be crive in and/or immediately adjacent to certain specified cell or tissue abnormalities. This sequence is a substrate for cathespin D. These sequences can be used in the conjugate system of the invention.

These sequences can be used in the conjugate system of the invention. The conjugate system is for delivering a therapeutic or dapprostic agent to a tissue abnormality site (ThS) in a patient. The system comprises a lipophilic or amphiphilic agent, covalently linked to a protease a sensitive polypeptide (such as this sequence) having an amino acid sequence readily cleavable by a protease active at the TAS, but not at a compalities use is a solubility modifier conjugated to the protease sensitive polypeptide. Peptides sensitive to cleavage by bacterial collagenase. They IV (also known as 72 kd galatinase, mammalian matrix proteinase-1, or MMP-2), or mesoporphyrin IX, can also be used in the caused by malignancy, tissue allymies, intravascular or extravascular collagenase by malignancy, tissue injuries, intravascular or extravascular collagenase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enzyme substrate; MMP-1; protease; tissue abnormality; mesoporphyrin IX; mailynancy; mammalian matrix metalloproteinase; buman interstitial collagenase; cathespin D; plasmin; fungal infection; human collagenase; cathespin D; plasmin; fungal infection; human collagenase Type IV; mammalian matrix proteinase-2; tissue injury; 72 K gelatinase; MMP-2; intravascular clotting; bacterial infection; parasitic infection.
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conjugate system for delivering therapeutic or diagnostic agent to tissue abnormality site - useful to treat or detect abnormalities caused by, e.g. malignancy or tissue injuries
                                                                                            0;
                                               Score 25, DB 19; Length 8; Pred. No. 7.8e+05; i. Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pottier RH, Ringuet M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5; Column 18; 10pp; English.
                                                                                                                                                                                                                                                                                                     AAW17691 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Substrate #1 for cathespin D.
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92US-0833183.
                                               59.5%;
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                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                             Query Match
Best Local Similarity 80.0.
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8 AA;
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05-OCT-1990;
10-FEB-1992;
                                                                                                                                         4 HLYIL 8
                                                                                                                                                                      |||:|
2 HLYLL 6
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                                                                                                                                                                                                                                                                                                                                                                                            07-JUL-1997
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                                                                                                                                                                                                                                                                                                                                                  AAW17691;
       Seguence
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Thu Dec 19 16:45:38 2002

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The invention relates to a method for determination of the amino acid sequence of an unknown peptide. The method comprises (a) determining the molecular mass and an experimental fragmentation spectrum for the molecular mass and theoretical fragmentation spectrum of the peptide; (b) comparing the experimental fragmentation spectrum for the unknown peptide with a theoretical fragmentation spectra calculated for a peptide intrary composed of all possible linear sequences of amino acids having a total mass that corresponds to the molecular mass of the unknown peptide; and (c) identifying a peptide in the library with a theoretical fragmentation spectrum that most closely matches the tragmentation spectrum of the unknown peptide. The method is useful in DNA cloning, anti-body production, identification of recombinant products, and the study of post-translational modifications. It allows the sequence of unknown peptides or proteins with no sub-sequence identity, to be characterised using mass spectrometry Sequences and the method. The isoleucine residue in these peptides can be replaced by leucine to construct another 264 linear peptides to be included in the library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method for determination of the amino acid asquence of an unknown peptide. The method comprises (a) determining the molecular mass and an experimental fragmentation spectrum for the peptide; (b) comparing the experimental fragmentation spectrum of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid determination; molecular mass; fragmentation spectrum; DNA cloning; anti-body; recombinant; modification; mass spectrometry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide sequence determination used in e.g. DNA cloning - by comparing mass spectra of the unknown peptide with a library linear chain known peptide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 23; DB 19; Length 6;
Pred. No. 7.8e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide determined by the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Townsend RR, Wedd NS;
          linear chain known peptide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
                                                     Example 1; Page 20; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 20; 40pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-571195/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-MAY-1997;
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2 GHIY 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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Matches
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AAW87172
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          E X & X D O O O O O O O O O O O O O O O O X &
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                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a process for preparation of short length peptides by culture of a transformant with an expression vector. Prepared by insertion of a gene encoding the fused peptide with the short peptide and the selective enzyme cleavage site, containing 2 or more genes encoding for a fused peptide with a short length peptide, particularly containing a histidine tag, and a selective enzyme followed by cleavage with the enzyme recognising the selective enzyme cleavage site. The method involves selective cleavage of jung cleavage site. The method involves selective cleavage of long cleavage to give the aimed short length peptide. The present sequence is a peptide derived from the ACE protein (not defined) suitable for production using the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid determination; molecular mass; fragmentation spectrum; DNA cloning; anti-body; recombinant; modification; mass spectrometry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                         A process for preparation of short length peptides by culture of a transformant with an expression vector, followed by cleavage with an enzyme recognising the selective enzyme cleavage site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 24; DB 23; Length 8; Pred. No. 7.8e+05; 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide determined by the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Townsend RR, Wedd NS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 9; 12pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW87243 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57.18;
                                                                                                                                    13-OCT-2000; 2000JP-0313609.
                                                                                       13-OCT-2000; 2000JP-0313609.
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                                                                                                                                                                                       (TOHA-) TOYO HAKKO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Parekh RB, Prime SB,
                                                                                                                                                                                                                                 WPI; 2002-475328/51.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8 AA;
JP2002119284-A.
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1 ISHIYV 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-FEB-1999
                                               23-APR-2002.
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Matches
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The invention relates to a method for determination of the amino acid sequence of an unknown peptide. The method comprises (a) determining the molecular mass and an experimental fragmentation spectrum for the peptide: (b) comparing the experimental fragmentation spectrum of the unknown peptide with a theoretical fragmentation spectra calculated for a peptide library composed of all possible linear sequences of amino acids having a total mass that corresponds to the molecular mass of the unknown peptide; and (c) identifying a peptide in the library with a theoretical fragmentation spectrum that most closely matches the fragmentation spectrum of the unknown peptide. The method is useful in pink cloning, anti-body production, identification of recombinant products, and the study of post-translational modifications. It allows
            The C-terminal is amidated. The peptide is an example of a highly generic formula for bombesin antagonists which are [psi8-9 pseudo] tomospeptides control.

2.3.4.9-tetrahydro-iH-pyrido(13.4-b)-indo1-3-carboxylic acid (Tpi) at the N- and/or C-terminal (3.4-b)-indo1-3-carboxylic acid (Tpi) at the peptide is a bombesin/GRP (gastrin releasing peptide) antagonist and is useful for treatment of states of hypergastrinemia, e.g. pernicious anaemia, chronic atrophic gastriis, zollinger-Ellison syndrome and vitiligo, associated with diffuse hyperplasia of gastric enterochromaffin-like cells, and with an increased risk of developing multifocal gastric carcinoid tumours. The peptide can also be used to treat lung, colon and gastric cancers. Dosage is 1-1000 mircrog/Kg parenterally.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid determination; molecular mass; fragmentation spectrum; DNA cloning; anti-body; recombinant; modification; mass spectrometry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide sequence determination used in e.g. DNA cloning - by comparing mass spectra of the unknown peptide with a library of linear chain known peptide sequences
                                                                                                                                                                                                                                                                                                54.8%; Score 23; DB 13; Length 8; 60.0%; Pred. No. 7.8e+05; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide determined by the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parekh RB, Prime SB, Townsend RR, Wedd NS;
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                                                                                                                                                                                                                                                                                                                                    Conservative
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Best Local Similarity
' hea 3; Conserve
                                                                                                                                                                                                                                                                8 AA;
                                                                                                                                                                                                                                                                                                                                                                    2 IGHLY 6
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4 VGHLW 8
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unknown peptide with a theoretical fragmentation spectra calculated for a peptide library composed of all possible linear sequences of amino acids having a total mass that corresponds to the molecular mass of the unknown peptide; and (c) identifying a peptide in the library with a theoretical fragmentation spectrum that most closely matches the fragmentation spectrum of the unknown peptide. The method is useful in DNA cloning, anti-body production, identification of recombinant the sequence of unknown peptides or proteins with no sub-sequence identify, to be characterised using mass spectrometry. Sequences identify, to be characterised using mass spectrometry. Sequence of sexpality the method. The isoleucine residue in these peptides constructed to exemplity the method. The isoleucine residue in these peptides can be included in the library.
                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= psi
/note= "Trp(For), For= formyl; residues 7-8 are
linked via a pseudo peptide bond"
                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label- psi
/note= "residues 7-8 are linked via a pseudo
peptide bond"
                                                                                                                                                                                                                                                                                                Score 23; DB 19; Length 6; Pred. No. 7.8e+05; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Mpp-Gln; Mpp= 3-(4-methoxyphenyl)
propionic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bombesin; GRP; gastrin releasing peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 8; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR28459 standard; Protein; 8 AA.
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Best Local Similarity 75.0%;
Matches 3; Conservative
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                                                                                                                                                                                                                                                                  6 AA;
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                      3 GHLY 6
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AAW60303-89 represent peptides recovered from human breast cancer. The peptides are tumour homing peptides, and are identified by in vivo panning. The in vivo panning comprises administering a library of diverse peptides to a subject having a tumour, collecting a sample of the tumour, identifying a peptide that fowes to the tumour, ollecting a sample of cormal tissue corresponding to the tumour, and determining that the peptide that homes to the tumour, and determining thissue. The tumour homing peptides can be linked to a moiety (e.g. doxorubicin), and used to direct the moiety to a tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumour homing molecules and their conjugates – useful for, e g. directing linked molety to tumour containing anglogenic vasculature
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                                           Score 22; DB 19; Length 6;
Pred. No. 7.8e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumour homing peptide; in vivo panning; alpha-V-containing integrin binding motif; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumour homing peptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                    AAW60362 standard; peptide; 7 AA.
                                           52.4%;
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                                                                                                              Conservative
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3 RTGHL 7
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                                                                                                                                                                                                                          1 IGHEY
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                                                                                                                                                                                                                                                                                                                                                                                    ó
the sequence of unknown peptides or proteins with no sub-sequence identity, to be characterised using mass spectrometry. Sequences AAM87101 to AAM87104 represent a library of linear peptides constructed roexemplify the method. The isoleucine residue in these peptides can be replaced by leucine to construct another 264 linear peptides to be included in the library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid determination; molecular mass; fragmentation spectrum; DNA cloning; anti-body; recombinant; modification; mass spectrometry.
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                         Score 22; DB 19; Length 6;
Pred. No. 7.8e+05;
); Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                 52.4%;
ilarity 80.0%;
Conservative
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Best Local Similarity
Matches 4; Conserv
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Gaps

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This invention describes novel peptides which home to angiogenic vasculature, specifically of a tumour and which have anti-tumour, anti-inflammatory, anti-angiogenic and anti-arthritic activity. Such anti-inflammatory, anti-angiogenic and anti-arthritic activity. Such molecules are identified by treating a purified MGR receptor with a test compound and identifying compounds that bind specifically to the NGR receptor. The peptides of the invention are inhibitors of angiogenesis and can be used to produce conjugates for delivering agents to angiogenic vasculature, particularly anticancer drugs or an imaging or an imaging or an imaging agent, for diagnosis or prognosis. These conjugates may be directed to non-tumour angiogenic vasculature, e.g. that present in inflammatory, regenerating or wounded tissue, e.g. for treatment of macular egenerating or wounded tissue, e.g. for treatment of macular provide specific targeting to tumours, especially their supporting vasculature. Precise targeting should reduce the systemic toxicity of anticancer drugs in the conjugates. Complete killing of all may result in an occlusive thrombus, and endothelial cells are unlikely to become resistant to anticancer agents nor to lose the targeting receptor. AskW938612-W93809 and AWW93843-44 are examples of tumour homing peptides used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                Tumour homing peptide; tumour: diagnosis; endothelial cell; breast; angiogenic; asculature; anti-tumour; anti-inflammetory; anti-angiogenic; anti-arthritic; NGR receptor; inhibitor; angiogenesis; anticancer drug; prognosis; inflammation; regeneration; wounded tissue; targetting; macular degeneration; diabetic retinopathy; rheumatoid arthritis; occlusive thrombus; human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying molecules that home to angiogenic vasculature used as targets for anticancer agents
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  Human breast cancer derived tumour homing peptide 60.
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Job time : 40 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example II; Page 104; 180pp; English.
                                                                                                                                                                                                                                                                                                                                        98US-0139802.
                                                                                                                                                                                                                                                                                                  98WO-US18895
                                                                                                                                                                                                                                                                                                                                                                                                                                            Pasqualini R, Ruoslahti E;
                                                                                                                                                                                                                                                                                                                                                                                                       (BURN-) BURNHAM INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-215158/18.
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10-SEP-1997;
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3 RTGHL 7
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Perfect score: Scoring table:

Sequence:

Searched:

OM protein

Run on:

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ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptides and Their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMMITS: USA
CONTRY: USA
COMPUTE: 13834
COMPUTER: EDSNAM:
MEDIUM TYPE: Diskette
COMPUTER: EM COMPATIBLIA
OPERATING SYSTEM: DOS
CURRAT APPLICATION DATA:
RAPLICATION NUMBER: US/09/017,743C
FILING DATE: 03-FEb-199
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/017,743C
FILING DATE: 33-374-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Parent, Annette S. REGISTRATION NUMBER: 42,058 REFERENCE/DOCKET NUMBER: 018623-008050US
5-09-989-789-281

5-09-989-789-281

5-09-989-789-283

5-09-989-789-283

5-09-989-789-284

5-09-989-789-284

5-09-989-789-318

5-09-989-789-318

5-09-989-789-318

5-09-989-789-318

5-09-989-789-393

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5-09-989-789-393

5-09-989-789-413
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S-09-989-789-889
S-09-989-789-889
S-09-989-789-835
S-09-989-789-838
S-09-989-789-841
S-09-989-789-935
S-09-989-789-935
S-09-989-789-935
S-09-989-789-935
S-09-989-789-935
S-09-989-789-935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 100, Application US/09017743C
Patent No. US20202017769411
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
Sidney, John
Sidney, John
Southwood, Scott
TITLE OF INVENTION: HLA Binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
    NUMBER OF SEQUENCES:
  RESULT 1
US-09-017-743C-100
    Sequence 100, App
Sequence 1, Appli
Sequence 1, Appli
Sequence 16, Appli
Sequence 16, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 110, Appl
Sequence 117, Appl
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                                                                                                                       December 19, 2002, 16:57:45; search time 11 Seconds (without alignments) 12.192 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
2: cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
3: cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
4: cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
5: cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
6: cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
7: cgn2_6/ptodata/2/pubpaa/USO7_NEW_DUB.pep:*
8: cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
9: cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
10: cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
11: cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
11: cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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11: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
                   GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                      106657 seqs, 16763532 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                           - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1 RIGHLYIL 8
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Match Length
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Database :

Score

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Result

TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid

us-09-692-401-6.closed.rapb

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US-09-766-347-1
US-09-766-347-1
Sequence 1, Application US/09766347
Patent No. US20020169107A1
GENERAL INFORMATION:
APPLICANT: Rajagopalan, Raghavan
APPLICANT: Cantrell, Gary
APPLICANT: Dorshow, Richard
APPLICANT: Mallinckrodt Inc.
TITLE OF INVENTION: NOVEL AROMATIC AZIDES FOR TYPE I PHOTOTHERAPY
FILE REPERENCE: MRD-60
CURRENT APPLICATION NUMBER: US/09/766,347
CURRENT APPLICATION NUMBER: 2001-01-19
CURRENT APPLICATION NUMBER: 2001-01-19
NUMBER OF SEQ ID NOS: 1
SSEQ ID NO 1
LENGTH: 8
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Fatent No. US2002015090al
GENERAL INFORMATION:
FAPPLICANT: PIKE, IAN
TITLE OF INVENTION: HEPATITIS C VIRUS PEPTIDES
MUDRES OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
SADRESSEE: Saite 701-E Columbia Square
STREET: 555 13th Street, N. W.
CITY: Washington
STREET: D. C.
COUNTY: U. S.
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPAILS
COMPUTER: PATENTIN RELEASE #1.0, Version #1.30
CURREWARE: PATENTIN Release #1.0, Version #1.30
CURREWARE: PATENTIN RELEASE
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , OTHER INFORMATION: Bombesin analog US-09-766-347-1
                                                                                                                                                                                      Query Match
Best Local Similarity 75.0%;
Matches 3; Conservative
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-730-801-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Unknown
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LOCATION: (1)...(8
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; Patent No. US20020103132A1
; GENERAL INFORMATION:
    TITLE OF INVENTION: Reduction of Impairment of Respiratory Tract Mucosal
    TITLE OF INVENTION: Reduction of Impairment of Respiratory Tract Mucosal
    TITLE OF INVENTION: Tummuity
    TITLE OF INVENTION: Tummuity
    TITLE OF INVENTION: AUGUST
    CURRENT APPLICATION NUMBER: US/09/730,801
    CURRENT FILING DATE: 1998-04-28
    PRIOR PRILING DATE: 1998-04-28
    PRIOR PRILING DATE: 1998-04-28
    PRIOR APPLICATION NUMBER: US/09/067,032
    PRIOR RILING DATE: 1998-04-19
    PRIOR APPLICATION NUMBER: US/09/089
    PRIOR FILING DATE: 1996-04-19
    NOWARE OF SEQ. ID NOS: 1
    SEQ. ID NOT 1
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Sequence 10 VG20010046498A1

GENERAL INFORMATION.

APPLICANT: Rosalaht, Erki

APPLICANT: Pasqualini, Renata

APPLICANT: Pasqualini, Renata

APPLICANT: Bredesen, Dale E.

APPLICANT: Programmeric Prostate-Homing Peptides With

TITLE OF INVENTION: Chimeric Prostate-Homing Peptides With

TITLE OF INVENTION: Chimeric Prostate-Homing Peptides With

TILE REFERENCE: P-13 844

CURRENT APPLICATION NUMBER: US/09/165,086

CURRENT FILING DATE: 2000-01-21

PRIOR FILING DATE: 2000-01-21

NUMBER OF SEQ ID NOS: 235

SOFTWARE: FASSLERQ FOR Windows Version 4.0

SEGOID NO 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 52.4%; Score 22; DB 10; Length 7; Best Local Similarity 80.0%; Pred. No. 8.9e+04; Matches 4; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                             Query Match 64.3%; Score 27; DB 9; Length 8; Best Local Similarity 83.3%; Pred. No. 8.9e+04, Matches 5; Conservative 0; Mismatches 1; Indels Matches 5; Conservative 0; Mismatches 1; Indels
    STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-09-017-743C-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: synthetic peptide US-09-765-086-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                 2 IGHLYI 7
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3 RTGHL 7
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US-09-765-086-79
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US-09-730-801-1
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APPLICANT: SHERAAL, Linda A.

APPLICANT: SHERAAL, Linda A.

APPLICANT: SHERAAL, Linda A.

APPLICANT: USTGARTEN, JoSeph
TITLE OF INVENTION: RECOMBINANT CONSTRUCTS ENCODING
TITLE OF INVENTION: ANTIGENS
NUMBER OF SEQUENCES: A
ADDRESSE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW, suite 5500
COURRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW, suite 5500
COURTY: Washington
STATE: OF STREET: DISA
IPPE: DISK PETE OF STREET: DISK PETE OF STRE
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US-09-18-18-42
US-09-18-18-42
Sequence 42, Application US/09813718
Publication No. US20020182666A1
GENERAL INFORMATION:
APPLICANT: Schimmel. Paul
APPLICANT: Schimmel. Paul
APPLICANT: Wakasugi, Keisuke
TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
TITLE OF INVENTION: The Regulation of Angiogenesis
FILE REFERENCE: 00-221
CURRENT APPLICATION NUMBER: US/09/813,718
CURRENT FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 58
SOFTIAN 042
                                                                           Gaps
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Best Local Similarity 75.0%; Pred. No. 8.9e+04;
Matches 3; Conservative 1; Mismatches 0; Indels
                                                                       Indels
                                         Best Local Similarity 42.9%; Pred. No. 8.9e+04;
Matches 3; Conservative 3; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGG, RATE H
REGISTRATION NUMBER: 29, 959
REFERENCE/DOCKET NUMBER: 313
TELECOMOUNICATION INFORMATION:
TELEPHONE: 202-887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-09-813-718-42
                                                                                                                                2 IGHLYIL 8 :1 :1 :1 1 VGGVYLL 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 IGHL 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17, Application US/09756875
Fatent No. US20020150990A1
GENERAL INFORMATION:
TITLE OF INVENTION: HEPATITIS C VIRUS PEPTIDES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE SULLE 701-E Columbia Square
STREET: 555 13th Street, N. W.
CITY: Washington
STATE: D. C.
COUNTRY: U. S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIE: 2004
COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEW: PC-DOS/MS-DOS
OPERARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/756,875
FILING DATE:
PCLASSIFICATION:
PRIOR APPLICATION NUBBER: US 08/259,721
APPLICATION NUBBER: US 08/259,721
FILING DATE: 29-ANG-1994
APPLICATION NUBBER: PCT/GB93/00410
FILING DATE: 26-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENST, BARBARA G.
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 30,377
FELEPHONE: (202)/83-6040
INFORMATION FOR SEQ IN ON: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
"WUPF: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILLING DATE:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATE:

APPLICATION NUMBER: US 08/259,721

FILLING DATE: 29-40G-1994

APPLICATION NUMBER: PCT/GB93/00410

FILLING DATE: 26-FEB-1993

ATTORNEY/ACEWT INFORMATION:

NAME: ERNST, BARBARA G.

REGISTRATION NUMBER: 30,377

REFERNENCE/OCKET NUMBER: 1808-157A

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TRECENATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 annino acids

TYPE: annino acids

TYPE: annino acids

TOPPLOGGY: unknown

WOLECULE TYPE: peetide
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Best Local Similarity 42.9%;
Matches 3; Conservative
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TYPELGY: unknown
MOLECULE TYPE: peptide
US-09-756-875-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 IGHLYIL 8
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2 VGGVYLL 8
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US-09-756-875-17
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US-09-731-242A-24

Sequence 24, Application US/09731242A

Sequence 24, Application US/09731242A

Patent No. US20020058253A1

GENERAL INFORMATION:

APPLICANT: WITTRUP, K. DANE

APPLICANT: HOLLER, PHILLIP

TITLE OF INVENTION: HIGH AFFINITY TCR PROTEINS AND METHODS

FILE REFERENCE: 89-99

CURRENT APPLICATION NUMBER: US/09/731,242A

CURRENT APPLICATION NUMBER: US 09/09,338

PRIOR PILING DATE: 1999-12-06

PRIOR PILING DATE: 1999-12-06

PRIOR PILING DATE: 1999-12-06

NUMBER OF SEQ ID NOS: 53

SOFTWARE: 1998-01-20

NUMBER OF SEQ ID NOS: 53

LEGTH: 7

LEGTH: 7
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURREWY APPLICATION DATA:
APPLICATION NUMBER: US/09/824,286
FILING DATE: 02-Appr-2001
CLASSIFICATION ACURROWN>
PRIOR APPLICATION ACURROWN>
PRIOR APPLICATION ANTHER: 60/017,466
FILING DATE: 10-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: REDISK: RAPLAN, WALTEN A.
REGISTRATION NUMBER: 34,199
REGISTRATION NUMBER: 34,199
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAN: 617 679-2808
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 45.2%; Score 19; DB 10; Length 7; Best Local Similarity 66.7%; Pred. No. 8:94-04; Matches 4; Conservative 0; Mismatches 2; Indels Matches 4; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 45.2%; Score 19; DB 10; L Best Local Similarity 100.0%; Pred. No. 8.9e+04; Matches 3; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                       : LENGTH: 7 amino acids
: TYPE: amino acids
: TYPE: amino acid
: STRANDEDNESS: not relevant
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FRAGMENT TYPE: internal
: SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-824-286-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: misc_feature
LOCATION: ()..()
; OTHER INFORMATION: CDR3alpha sequence
US-09-731-242A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: ARTIFICIAL SEQUENCE
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4 HLY 6
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Sequence 14, Application US/09824286
Patent No. US2002002820241
GENERAL IMPORMATION:
APPLICANT BURKly, Linda C
Hessian, Catherine A
Whitty, Adrian
TITLE OF INVENTION: COMMON GAMMA CHAIN BLOCKING AGENTS
NUMBER OF SEQUENCES: 17
CORRESPONDENCES: 17
STREET: 14 Cambridge Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 45.2%; Score 19; DB 9; Length 7; Local Similarity 60.0%; Pred. No. 8.9e+04; nes 3; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                  Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9

US-10-060-100-86

Sequence 86, Application US/10080100

Patent No. US20020165356a1

GENERAL INFORMATION:

APPLICANT: Barbas, Carlos

APPLICANT: Dreler, Birgit

TITLE OF INVENTION: Zinc Finger Binding Domains for TITLE OF INVENTION: Langer Binding Domains for FILE REPERBURE: TSRI 760.0

CURRENT APPLICATION NUMBER: US/10/080,100

CURRENT FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 113

SOFTWARE: FESTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                Ouery Match

Query Match

45.2%; Score 19; DB 8; Le

Best Local Similarity 100.0%; Pred. No. 8.9e+04;

Matches 3; Conservative 0; Mismatches 0;
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ZIP: 02142
COMPUTER READABLE FORM:
MEDIUM TYPE: FlOPPY disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: synthesized US-10-080-100-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
  TELEFAX: 202-822-0168
TELEX:
TRECRATION FOR SEO ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 GHLYI 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 GHLRV 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
US-09-824-286-14
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Best Local S
Matches 3
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Gaps
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Sequence 45, Application US/09071838
Patent No. US20020152501A1
GENERAL INFORMATION
FISCHET, ROBERT L.
APPLICANT: Ohad, Nir
APPLICANT: Vadegari, Ramin
APPLICANT: Wargosslan, Linda
APPLICANT: Margosslan, Linda
APPLICANT: Margosslan, Linda
APPLICANT: Margosslan, Linda
APPLICANT: Margosslan, Linda
APPLICANT: Goldberg, Robert B,
TITLE OF INVENTION: Nucleic Acids That Control Seed and
TITLE OF INVENTION: Nucleic Acids That Control Seed and
TITLE OF INVENTION: Nucleic Acids That Control Seed and
STREET: The Embarcade and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STREET: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 45.2%; Score 19; DB 10; Length 8; Best Local Similarity 57.1%; Pred. No. 8.9er0, Marches 4; Conservative 2; Mismarches 1; Indels Matches 4; Conservative 2; Mismarches 1; Indels Mismarches 1; Indels Mismarches 2; Mismarches 1; Indels Mismarches 2; Mismarches 2; Mismarches 2; Mismarches 2; Mismarches 3; Mismarches 3; Mismarches 3; Mismarches 3; Mismarches 3; Mismarches 3; Mismarches 4; Mismarc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
US-10-080-100-83
US-10-080-100-83
Sequence 83. Application US/10080100
Fatent No. US20020165356A1
GENERAL INFORMATION
FAPLICANT: Defer Bigit
TILLE OF INVENTION: Birgit
TITLE OF INVENTION: Directide Sequence ANN
FITLE REFRENCE: TSRI 76.0
CURRENT FILING DATE: 2002-02-21
FRIOR PILING DATE: 2002-02-21
FRIOR APPLICATION NUMBER: US/9/791,106
FRIOR PILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 113
SOFTWARE FRASEEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA
APPLICATION NUMBER: US/09/071,838
FILING DATE: 01-MAY-1998
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        023070-086100US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATCHNEY/AGENT INFORMATION:
NAME: Bastlan, Kevin L.
REGISTRATION NUMBER: 4,774
REFERENCE/DOCKET NUMBER: 0230'
TELEPHONE: (415) 576-0200
ITELEPHONE: (415) 576-0200
ITELEPHONE: (415) 576-0200
ITELEPHONE: (415) 576-0200
INFORMATION FOR SED ID NO: 5EQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: peptide US-09-071-838-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                        APPLICANT: Poraces Pharmaceuticals, Inc.
APPLICANT: Wordsin, Benjamin
APPLICANT: Los of INVENTION: Micheal S.
TITLE OF INVENTION: WORDSIN: US/09/901,187B
CURRENT APPLICATION NUMBER: US/09/901,187B
PRIOR FILING DATE: 2000-07-07
PRIOR PAPLICATION NUMBER: US 60/217,319
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2001-07-28
SOFTWARE: Patentin version 3.1
SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10, Application US/09766889A

Patent No. US20020164654AI

GENERAL INFORMATION.
GENERAL INFORMATION.
GENERAL INFORMATION.
APPLICANT: Luiten, Rosalie
APPLICANT: Boon-Talleur. Thierry
APPLICANT: Boon-Talleur. Thierry
APPLICANT: Boon-Talleur. Therry
APPLICANT: Schultz, Ervin
TITE OF INVENTION WABER: William
FILE OF INVENTION MAER: US/09/766,889A
CURRENT ELING DATE: 2000-01-01-9
FRIOR FILING DATE: 2000-01-02
PRIOR FILING DATE: 2000-01-02
PRIOR FILING DATE: 2000-01-02
PRIOR FILING DATE: 2000-01-02
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ő
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                                                                              Sequence 10, Application US/09901187B Patent No. US20020151464A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
US-09-901-1878-10
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; ORGANISM: Homo sapiens
US-09-766-889A-10
    RESULT 12
US-09-901-187B-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
US-09-766-889A-10
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US-09-071-838-45
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; FEATURE:
; OTBEN INFORMATION: synthesized
US-10-080-100-83

Query Match

Query Match

Best Local Similarity 100.0%; Pred. No. 8.9e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GHL 5

Db 3 GHL 5

Db 3 GHL 5

Search completed: December 19, 2002, 17:01:39

Job time : 19 secs
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us-09-692-401-6.closed.rai

Scoring table:

Searched:

Database :

Perfect score:

Sequence:

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RESULT 1
US-08-529-190B-45
| Sequence 45, Application US/08529190B
| Sequence 45, Application US/08529190B
| Patent No. 583391
| GENERAL INFORMATION: GENERAL INFORMATION: GINCENATION: GINCENATION: GINCENATION: GINCENATION: GINCENATION: GINCENATION: GINCENATION: ONFERRING INVISIBILITY TO THE IMMUNE SYSTEM INVINERE OF SEQUENCES: 7
| CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESS: 3
| ADDRESSEE: Banner & Witcoff, Ltd. 5TREET: CORRESPONDENCE ADDRESS: 3
| ADDRESSEE: Banner & Witcoff, Ltd. 5TREET: CORRESPONDENCE ADDRESS | 3 CORRESPOND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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US-09-189-129-14
US-09-065A-2
US-09-03-3-34G-22
US-08-07-303-14
US-08-159-3-103A-14
US-08-159-3-103A-14
US-08-457-804-11
US-08-443-3-41-14
US-08-39-2-73E-14
US-08-39-2-73E-14
US-08-160-604-46
US-08-160-604-47
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: WORDER: DOS
SOTTWARE: WORDER: US/08/529,190B
FILING DATE: 15-8EP-1995
FILING DATE: 10-REP-1995
FILING DATE: 10-REP-1995
FILING DATE: 10-REP-1995
ATTORNEY/AGENT INVORMATION
NAME: WILLIAMS: NI-), KARTHLEEN ARESTERMEY/COKET NUMBER: 34,380
RESTERMENCE/DOCKET NUMBER: 34,380
TELECOMMUNICATION NUMBER: 34,380
TELECOMMUNICATION NUMBER: 34,380
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 45
SEQUENCE CHARACTERISTICS:
LENGTH: 8 anino acid
TYPE: anino acid
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Best Local Similarity 80.0
Matches 4; Conservative
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    Sequence 45, Appl.
Sequence 79, Appl.
Sequence 3, Appl.
Sequence 16, Appl.
Sequence 16, Appl.
Sequence 17, Appl.
Sequence 27, Appl.
Sequence 28, Appl.
Sequence 28, Appl.
Sequence 28, Appl.
Sequence 29, Appl.
Sequence 39, Appl.
Sequence 64, Appl.
Sequence 64, Appl.
Sequence 64, Appl.
Sequence 39, Appl.
Sequence 39, Appl.
Sequence 39, Appl.
Sequence 29, Appl.
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                                                                                                                                                                                                                                                                    December 19, 2002, 16:55:55; Search time 14 Seconds (without alignments) 16.813 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-08-131-897A-5
US-08-139-802-3
US-08-139-802-3
US-08-139-802-3
US-08-138-39-3
US-08-530-342A-15
US-09-067-032-1
US-09-067-032-1
US-09-18-390-11
US-08-18-390-11
US-08-18-390-13
US-08-18-390-13
US-08-18-390-13
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US-08-387-634-3
US-08-387-63-3
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US-08-014-979-80
US-08-177-109A-39
US-08-687-706-39
US-08-482-228-126
US-08-482-528-126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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42
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Match Length
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US-08-168 -390-3

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Pred. No. 1.9e+05;
1; Mismatches 0; Indels
Query Match 52.4%; Score 22; DB 4; Length 7; Best Local Similarity 80.0%; Pred. No. 1.9e+05; Matches 4; Conservative 0; Mismatches 1; Indels Matches 4; Annual Matches 4; Mismatches 4; Annual Matches 4; Conservative 0; Mismatches 1; Indels Matches 4; Conservative 0; Mismatches 1; Conservative 0; Conservative 0; Mismatches 1; Conservative 0; Conser
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COCATION: 7 Modified-site
OTHER INFORMATION: /note= "The carboxy-terminal
COTHER INFORMATION: residue comprises an ethyl ester.
US-08-168-390-3
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US-08-974-775-48
Sequence 48, Application US/08974775
Patent No. 6096706
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Best Local Similarity 75.0
Matches 3; Conservative
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3 RTGHL 7
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Sequence 79, Application US/09139802
Fatent No. 6180084
Fatent No. 6180084
Fatent No. 6180084

APPLICANT: Rucolahti, Erkki
APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: No. Receptor and Methods of Identifying Tumor Homing
TITLE OF INVENTION: Molecules That Home to Anglogenic Vasculature Using
TITLE OF INVENTION: Same
TITLE OF INVENTION: Same
FILE REFERENCE: P-LJ 3203
CURRENT EILNE MAPPLICATION NUMBER: US/09/139,802
CURRENT EILNE DATE: 1997-09-10
EARLIER APPLICATION NUMBER: 08/226,914
EARLIER APPLICATION NUMBER: 08/226,914
EARLIER FILING DATE: 1996-09-10
NUMBER OF SEQ ID NOS: 226
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 79
LENGTH: T
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-139-802-79
                                                                                                                                                                                                                                                                                NESULIA. 68-213-897A-5

SEQUENCE 5, APPLICATION US/08213897A

PATENT NO. 5618790

SEQUENCE INFORMATION:
APPLICAMY:
TITLE OF INVENTION: PROLease Mediated Drug Delivery System NUMBER OF SEQUENCES: 18

COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PRICATION DATA:
COMPUTER: PRICATION DATA:
APPLICATION NUMBER: US/08/213,897A

PRICATION NUMBER: US/08/213,897A

PRICATION NUMBER: US/07/593,867

FILING DATE: 05-0CT-1990

PRICATION NUMBER: US/07/593,867

FILING DATE: 10-FEB-1992

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: Amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-213-897A-5
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2 GHFFVL 7
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                                           4 HLYIL 8
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2 HLYLL 6
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US-09-139-802-79
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US-09-473-355-1

US-09-473-355-1

Sequence 1, Application US/09473355

Patent No. 6262027

SEQUENCEL INFORMATION:

TITLE OF INVERTION:

FILE REFERENCE: 44137-5001-02-US

CURRENT FILIC OP INVERTION NUMBER: US/09/473,355

CURRENT FILIC DATE: 1999-12-28

EARLIER APPLICATION NUMBER: US (09/067,032

EARLIER APPLICATION NUMBER: US (08/4842,877

EARLIER APPLICATION NUMBER: US (08/4842,877

EARLIER APPLICATION NUMBER: US (06/029,689

EARLIER FILING DATE: 1996-10-31

SERVIER APPLICATION NUMBER: US (06/029,689

EARLIER FILING DATE: 1996-04-19

NUMBER OF SEQ ID NOS: 1

SEQ ID NOS: 1

SEQ ID NOS: 1

SEC ID NOS: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.0%; Score 21; DB 4; Length 7; 66.7%; Pred. No. 1.9e+05; Live 1; Mismatches 1; Indels
            SOFTWARE: WordPerfect for Windows 6.0a CURRENT APPLICATION DATA.
APPLICATION DATA.
APPLICATION DATA.
FILING DATE: 08-MAR-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DE94/00370
FILING DATE: 29-MAR-1994
APPLICATION NUMBER: P 43 11 022.3
ATTORNEY/ACENT INFORMATION:
NAME: MOTTIME: JOHN 8.30
RESISTRATION NUMBER: 30,407
REFERENCE/COCKET NUMBER: 1214.00008
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear NOLOGULE TYPE: peptide HYPOPHETICAL: NO ANTI-SENSE: NO FRAGNET TYPE: N-terminal CORGINAL SOURCE: US-08-530-342A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Bombina bombina
US-09-473-355-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 4; Conserve
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| GHLDII 6
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| Sequence 15, Application US/08530342A
| Patent No. 6143275
| GENERAL INFORMATION:
| APPLICANT: DIRRELBORG, LUDGER
| APPLICANT: DIRRELBORG, LUDGER
| APPLICANT: SCHIER, WOLGANG
| APPLICANT: SCHIER, WOLGANG
| APPLICANT: SCHIER, WOLGANG
| TITLE OF INVENTION: TYPE SINC CHELATORS FOR RADIO
| TITLE OF INVENTION: TYPE ISOTOPES, THEIR METAL COMPLEXES AND TITLE OF INVENTION: THEIR DIAGNOSTIC AND THERRAPEUTICAL USE
| TITLE OF INVENTION: THEIR DIAGNOSTIC AND THERRAPEUTICAL USE
| CORRESPONDENCES: SCHOOL AND SHILLIPS, VAN SANTEN, CLARK & ADDRESSEE: WOOD, PHILLIPS, VAN SANTEN, CLARK & STREET: SOOW West Madison Street, Suite 3800
| CITY, Chicago
GENERAL INFORMATION:
APPLICANT: TODACK, F. GATY
APPLICANT: TODACK, F. GATY
TITLE OF INVENTION: GROWTH-PROMOTING PROTEINS AND PEPTIDES
TITLE OF INVENTION: FOR KIDNEY EPITHELIAL CELLS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC TOWAR - Suite 3600, 455 N. Cityfront
STREET: NBC TOWAR - Suite 3600, 455 N. Cityfront
STREET: NBC TOWAR - Suite 3600, 455 N. Cityfront
STREET: NBC TOWAR - Suite 3600, 455 N. Cityfront
STREET: NBC TOWAR - Suite 3600, 455 N. Cityfront
STREET: NBC TOWAR - Suite 3600, 455 N. Cityfront
STREET: NBC TOWAR - Suite 3600, 455 N. Cityfront
STREET: NBC TOWAR - Suite 3600, 455 N. Cityfront
STREET: Illinois
COUNTRY: Chicago
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IMP PC COMPATA:
MEDIUM TYPE: Patentin Release #1.0, Version #1.30
COMPUTER: DATE: 20 NOV-1997
CLASSIFICATION NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 35,601
TELEBHONE: 312-321-4209
TELEBHONE: 312-321-4209
TELEBHONE: 312-321-4209
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ZIP: 6061-211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: COMPAO Prolinea 4/25s
OPREATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 312-321-4299
INFORMATION POR SEQ. ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
STRANDENRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-974-775-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IL
USA
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US-08-530-342A-15
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3 VGHL 6
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Gaps
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APPLICANT: Takahashi, Kazayuki
APPLICANT: Takahashi, Kasayuki
APPLICANT: Takahashi Sombesin/Gastrin Releasing Peptide Antagonists
TITLE OF INVENTION: Bombesin/Gastrin Releasing Peptide Antagonists
TITLE OF INVENTION: Bombesin/Gastrin Releasing Peptide Antagonists
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
Nodified-site
LOCATION: Modified-site
LOCATION: Comprises one of several chemical end caps."
OTHER INFORMATION: Comprises one of several chemical end caps."
FEATURE:
NAME/KEY: Modified-site
'CONTION: 8 'CONTION: 9 'CONTION: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50.0%; Score 21; DB 6; Length 7; ilarity 75.0%; Pred. No. 1.9e+05; Conservative 1; Mismatches 0; Indels
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O'THER INFORMATION: /note= "The carboxy-terminal
; O'THER INFORMATION: residue comprises an ethyl ester."
US-08-168-390-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY READABLE FORM:
COUNTRR READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC COMPOS/MS-DOS
SOFTWARE: PARCHILI RC-GS/MS-DOS
SOFTWARE: PARCHILI RC-GS/MS-DOS
SOFTWARE: DATORNARE: US/08/168,390
FILING DATE: Herewith
FALICATION NUMBER: US/08/168,390
FILING DATE: HEREWIT INFORMATION:
NAME: GOLGSTEIN, US/08 A.
REGISTRATION NUMBER: US/1.040001
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEC ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 mainto acids
TYPE: aminto ACIDS
TYPE: AMINDO ACIDS
TYPE: AMINDO ACIDS
TYPE: AMINDO ACIDS
TYPE: AMINDO ACIDS
APPLICATION NUMBER: US/08/47,006
FILING DATE: 15-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 695,004
FILING DATE: 03-MAY-1991
APPLICATION NUMBER: 281,951
FILING DATE: 05-EC-198
FILING DATE: 05-DEC-198
FILING DATE: 05-DEC-1988
APPLICATION NUMBER: 717,692
FILING DATE: 29-MAR-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application US/08168390
Patent No. 5620955
GENERAL INFORMATION:
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Matches 3; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : | | |
3 VGHL 6
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US-08-168-390-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                    ;SEQ ID NO:3
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                                                                                                                                                                                                                                                                                                             APPLICANT: Kudsk, Kenneth A.
TITLE OF INVENTION: Reduction of Impairment of Respiratory Tract Mucosal
TITLE OF INVENTION: Reduction of Impairment of Respiratory Tract Mucosal
TITLE OF INVENTION: Immunity
RILE REFERENCE: 44137-5001-01-05
CURREMY PELLIAND NUMBER: US/09/067,032
CURREMY PELLIAND NUMBER: US/08/067,032
CURREMY PELLIAND NUMBER: US/08/08/28
EARLIER APPLICATION NUMBER: US/08/08/28
EARLIER APPLICATION NUMBER: US/06/029,689
EARLIER APPLICATION NUMBER: US/06/029,689
EARLIER APPLICATION NUMBER: US/06/029,689
EARLIER FILING DATE: 1996-10-31
SARLIER FILING DATE: 1996-10-31
SOFTWARE: Patentin Ver: 2.1
SSOFTWARE: Patentin Ver: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
5217955.
5217955.
7 PATENT NO. 5217955
7 PATENT NO. 5217955
7 PATENT NO. 5217955
7 PAPLICANT: aBOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE
7 POMBESIN, GRP, LITORIN OR NEUROMEDIN
8 NUMBER OF SEQUENCE: 42 NEUROMEDIN
8 NUMBER OF SEQUENCE: 42
8 PELING DATE: 09-MAX-1990
9 FILING DATE: 09-MAX-1990
9 FILING DATE: 10-MAX-1990
9 FILING DATE: 11-NOV-1989
9 FILING DATE: 21-NOV-1989
9 FILING DATE: 15-SEP-1989
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5460801-3
; PATENT NO. 5460801
; TILE OF INVENTION OF SMALL CELL LUNG CANCER CELL;
; GROWITH IN VIVO USING MONOCLONAL ANTIBODY
; NUMBER OF SEQUENCES: 3
; CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 50.0%; Score 21; DB 4; Length 7; Best Local Similarity 75.0%; Pred. No. 1.9e+05; Matches 3; Conservative 1; Mismatches 0; Indels Matches 1; Conservative 1; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.0%; Score 21; DB 6; Length 7;
llarity 75.0%; Pred No. 1.9e+05.
Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                           Sequence 1, Application US/09067032
Patent No. 6271202
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-067-032-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 3; Conserv
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3 VGHL 6
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; LENGTH: 7
5217955-30
    3 VGHL 6
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3 VGHL 6
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US-09-067-032-1
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OTHER INFORMATION:
OTHER INFORMATION: The sequence contains at position 1 an acetylated His, rat.
OTHER INFORMATION: than a His, and has an amide C-terminus (i.e., COOH).
US-08-387-634-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 50.0%; Score 21; DB 1; Length 8; Best Local Similarity 75.0%; Pred. No. 1.9e+05. Matches 0; Indels Matches 0; Indels
   GENERAL INFORMATION:
APPLICANT: Kim, Sun Hyuk
APPLICANT: Moreau, Jacques-Pierre
APPLICANT: Moreau, Jacques-Pierre
TITLE OF INVENTION: LINEAR THERAPEUTIC PEPTIDES
TUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                      STATE: Massachusetts

COUNTRY: Massachusetts

COUNTRY: U.S.A.
ZIPE: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Diskette, 1.44 Mb
CCMPUTER: TBW PS/2 Model 502 or 5530

COMPUTER: TBW PS/2 Model 502 or 5530

CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/387,634

FILING DATE: 08/09/90

ATTRING DATE: 05/09/90

TELEPROME: (017) 542-8906

TELEPROMUNICATION INPORMATION:
TELEPROME: (017) 542-8906

TELEPROMUNICATION INPORMATION:
TELEPROMO FOR SED ID NO: 3:
SEDURICE CHARACTERISTICS:
LENGTH: 617

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US-08-337-127-9
US-08-337-127-9
Sequence 9, Application US/08337127
Sequence 9, Application US/08337127
GENERAL INFORMATION:
APPLICANT: COY, David H.
APPLICANT: Moreau, Jacques-Pierre
APPLICANT: Kim, Sun H
TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN
TITLE OF INVENTION: ANALOGS
NUMBER OF SOUGHNESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 225 Franklin S
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
FEATURE:
                                                                                                                                                                                          STREET: 225 F1
CITY: Boston
STATE: Massach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 IGHL 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                              .,
   50.0%; Score 21; DB 1; Length 8; 75.0%; Pred. No. 1.9e+05; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: /note= "The carboxy-terminal OTHER INFORMATION: residue comprises an ethyl ester." US-08-168-390-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 50.0%; Score 21; DB 1; Length 8; Best Local Similarity 75.0%; Pred. No. 1.9e+05; Matches 0; Indels Matches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-08-387-634-3
; Sequence 3, Application US/08387634
; Patent No. 5767236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Modified-site LOCATION: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: Modified-site
LOCATION: 8
Query Match
Best Local Similarity 75.0
Matches 3; Conservative
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                                                                                                            2 IGHL 5
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5 VGHL 8
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US-08-168-390-13
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Query Match
50.0%; Score 21; DB 4; Length 8;
Best Local Similarity 42.9%; Pred. No. 1.9e+05;
Matches 3; Conservative 3; Mismatches 1; Indels
                                                                                          STATE: CANADIA COLOR STREET
STATE: CANADIA COUNTRY: USA
ZIP: 94608-2916
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIALE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: PATENTE RECENT NO. Version #1.30
CUNREWN APPLICATION DATA:
APPLICATION NUMBER: US/08/44,818
FILING DATE: CASSIFICATION DATA:
PRIOR PAPLICATION NUMBER: US/08/403,590
FILING DATE: 14-MAR-1995
ATTORREY AGENT INFORMATION:
NAME: HAIDIN, Alisa A.
REGISTRATION NUMBER: 0110.002
TELECOMMUNICATION NUMBER: 0110.002
TELECOMMUNICATION NUMBER: 0110.002
TELECOMMUNICATION TORORANTION:
TELEFAX: (508)359-3885
INFORMATION FOR SEQ ID NO: 258:
SECURENCE CHARACTERISTICS:
LENGTH: 80 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 completed: December 19, 2002, 16:58:35
ne : 29 secs
   CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: peptide US-08-444-818-258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 IGHLYIL 8
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Job time
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Patent No. 6150087
GENERAL INFORMATION:
APPLICANT: Chien, David Y.
APPLICANT: Rutter, Milliam J.
TITLE OF INVENTION: NANBY Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                    PELLING DATE:

CLASSIFICATION: 530
PRICK APPLICATION DATA:

APPLICATION NUMBER: 07/779,039
FILING DATE: 10/18/91
APPLICATION NUMBER: 07/502,438
FILING DATE: 03/30/00
APPLICATION NUMBER: 07/30/169
FILING DATE: 08/21/89
APPLICATION NUMBER: 07/316,555
FILING DATE: 07/30/28
APPLICATION NUMBER: 07/316,328
FILING DATE: 03/30/28
APPLICATION NUMBER: 07/28/328
FILING DATE: 09/28/88
APPLICATION NUMBER: 07/28/328
FILING DATE: 09/28/88
APPLICATION NUMBER: 07/28/318
APPLICATION NUMBER: 07/20/13/89
FILING DATE: 09/28/88
APPLICATION NUMBER: 07/20/4/11
FILING DATE: 09/28/88
APPLICATION NUMBER: 07/20/4/11
FILING DATE: 09/28/88
APPLICATION NUMBER: 07/20/13/311
FILING DATE: 09/28/88
APPLICATION NUMBER: 07/20/4/11
FILING DATE: 09/28/88
APPLICATION NUMBER: 07/10/571
FILING DATE: 09/28/88
APPLICATION NUMBER: 00/10/571
FILING DATE: 09/28/88
APPLICATION NUMBER: 00/28/88
APPLICATION NUMBER: 00/28
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
US-08-337-127-9
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TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
US-08-444-818-258
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5 VGHL 8
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